

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 17:31:33 ; Search time 7014.33 Seconds
(without alignments)
10680.938 Million cell updates/sec

Title: US-10-670-454-1
Perfect score: 1318
Sequence: 1 gttctctcttaccctgt.....caaaaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_ste.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1318	100.0	1318	6	BD243009	BD243009 Enzyme. 7
2	1318	100.0	1318	6	AR444991	AR444991 Sequence
3	1318	100.0	1318	6	AX008671	AX008671 Sequence
4	1316.4	99.9	1318	15	PC0132438	AJ132438 Phaseolus
5	1110.8	84.3	1360	15	AB181372	AB181372 Vigna ang
6	999	75.8	999	6	CQ899251	CQ899251 Sequence
7	893.8	67.8	1359	6	AR528429	AR528429 Sequence
8	484.6	36.8	1406	15	AV588978	AV588978 Nerium ol
9	464.4	35.2	1245	15	AV594292	AV594292 Nerium ol
10	462.2	35.1	1383	15	CMA315663	AJ315663 Cucurbita
11	459	34.8	1308	15	CWA302041	AJ302041 Cucurbita
12	453	34.4	1292	15	AB125232	AB125232 Nicotiana
13	439	33.3	1479	15	MMV09113	Y09113 M.macrocarp
14	430.8	32.7	1352	6	AR452821	AR452821 Sequence
15	429.2	32.6	1365	6	AR452817	AR452817 Sequence
16	427.6	32.4	1299	15	AB181373	AB181373 Vigna ang
17	426.2	32.3	1292	15	AB031206	AB031206 Lactuca s
18	425.8	32.3	1057	15	BT004464	BT004464 Arabidops

19	425.8	32.3	1223	15	ATH132436	AJ132436 Arabidops
20	425.8	32.3	1237	6	BD243013	BD243013 Enzyme. 7
21	425.8	32.3	1237	6	AR444995	AR444995 Sequence
22	425.8	32.3	1237	6	AX008677	AX008677 Sequence
23	425.8	32.3	1424	15	BT002987	BT002987 Arabidops
24	425.4	32.3	1026	6	AX506555	AX506555 Sequence
25	425.4	32.3	1026	6	AX651428	AX651428 Sequence
26	424.8	32.2	1403	6	AR528430	AR528430 Sequence
27	421	31.9	1306	15	AB125233	AB125233 Nicotiana
28	419.6	31.8	1324	15	AF056935	AF056935 Pisum sat
29	409.8	31.1	1277	15	AF100955	AF100955 Pisum sat
30	406.6	30.8	1229	15	AF506281	AF506281 Spinacia
31	402.6	30.5	983	15	AF101382	AF101382 Pisum sat
32	382.8	29.0	1008	6	BD243014	BD243014 Enzyme. 7
33	382.8	29.0	1008	6	AR444996	AR444996 Sequence
34	382.8	29.0	1008	6	AX008679	AX008679 Sequence
35	382.8	29.0	1008	15	ATH132437	AJ132437 Arabidops
36	380.2	28.8	1259	15	AB067639	AB067639 Daucus ca
37	363.6	27.6	1473	6	AR452818	AR452818 Sequence
38	363.6	27.6	1473	15	BT009225	BT009225 Trifolium
39	356.6	27.1	1021	15	BT002763	BT002763 Arabidops
40	356.6	27.1	1224	15	AY085539	AY085539 Arabidops
41	356.6	27.1	1316	15	ATH132435	AJ132435 Arabidops
42	356.6	27.1	1318	6	BD243012	BD243012 Enzyme. 7
43	356.6	27.1	1318	6	AR444994	AR444994 Sequence
44	356.6	27.1	1318	6	AX008675	AX008675 Sequence
45	355.6	27.0	1651	15	AK060666	AK060666 Oryza sat

ALIGNMENTS

RESULT 1	BD243009	1318 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD243009				
DEFINITION	Enzyme..				
ACCESSION	BD243009.1	GI:33052779			
VERSION	JP 2002518005-A/1.				
KEYWORDS	Phaseolus coccineus				
SOURCE	Phaseolus coccineus				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.				
REFERENCE	1 (bases 1 to 1318)				
AUTHORS	Thomas,S.G., Hedden,P. and Phillips,A.L.				
TITLE	Enzyme				
JOURNAL	Patent: JP 2002518005-A 1 25-JUN-2002;				
	THE UNIVERSITY OF BRISTOL				
COMMENT	OS Phaseolus coccineus (scarlet runner bean)				
	PN JP 2002518005-A/1				
	PD 25-JUN-2002				
	PF 11-JUN-1999 JP 2000554838				
	PR 12-JUN-1998 GB 9812821.8,15-JUL-1998 GB 9815404.0 PI				
	STEPHEN GREGORY THOMAS,PETER HEDDEN,ANDREW LEONARD PHILLIPS PC				
	C12N9/04,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10, PC				
	C12N15/09,				
PC	C12N5/00,C12N5/00,C12N15/00				
CC	Enzyme				
FH	Key				
FT	source				
	1. .1318				
	/organism='Phaseolus coccineus (scarlet runner bean)'				
FEATURES	Location/Qualifiers				
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	/mol_type="genomic DNA"				
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QY	1	GTTCCTCTCCCTTACCCCTGTTCTGCTTCTCTTTTTCATAGTAACAATCGACAACAAC	60						
Db	1	GTTCCTCTCCCTTACCCCTGTTCTGCTTCTCTTTTTCATAGTAACAATCGACAACAAC	60						
QY	61	AACAACCATGGTTGTTCTGCTCAGCGCAGCATGAACCAAGTTTCTCTCTGAAACCAT	120						
Db	61	AACAACCATGGTTGTTCTGCTCAGCGCAGCATGAACCAAGTTTCTCTCTGAAACCAT	120						
QY	121	CAAGTCCACGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCACGCCCCCGATGCCAA	180						
Db	121	CAAGTCCACGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCACGCCCCCGATGCCAA	180						
QY	181	GAATCTCATAGTAACGCCCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT	240						
Db	181	GAATCTCATAGTAACGCCCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT	240						
QY	241	TCCATTTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCA	300						
Db	241	TCCATTTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCA	300						
QY	301	GTCCGAGAAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGGTAGCAAGAGATTGG	360						
Db	301	GTCCGAGAAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGGTAGCAAGAGATTGG	360						
QY	361	CCCAACCGGTGATGTGGTGGGTGAATACCTCTCTCAACACCAACCCCTGATGTTAT	420						
Db	361	CCCAACCGGTGATGTGGTGGGTGAATACCTCTCTCAACACCAACCCCTGATGTTAT	420						
QY	1021	AGCTGATAATAGGCTTGCCTTTCCAGAAATCTGCTGCTGATTAACCAAAACACACCCCTT	1080						
RESULT 2									
AR444991									
LOCUS									
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
GBX;									
FEATURES									
source									
ORIGIN									
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Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GTTCCTCTCTTACCCCTGTTCTGCTTCTCTTTTTCATAGTAACAATCGACAACAAC	60						
Db	1	GTTCCTCTCTTACCCCTGTTCTGCTTCTCTTTTTCATAGTAACAATCGACAACAAC	60						
QY	61	AACAACCATGGTTGTTCTGCTCAGCGCAGCATGAACCAAGTTTCTCTCTGAAACCAT	120						
Db	61	AACAACCATGGTTGTTCTGCTCAGCGCAGCATGAACCAAGTTTCTCTCTGAAACCAT	120						
QY	121	CAAGTCCACGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCACGCCCCCGATGCCAA	180						
Db	121	CAAGTCCACGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCACGCCCCCGATGCCAA	180						
QY	181	GAATCTCATAGTAACGCCCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT	240						
Db	181	GAATCTCATAGTAACGCCCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT	240						
QY	241	TCCATTTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCA	300						
Db	241	TCCATTTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCA	300						
QY	301	GTCCGAGAAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGGTAGCAAGAGATTGG	360						
Db	301	GTCCGAGAAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGGTAGCAAGAGATTGG	360						
QY	361	CCCAACCGGTGATGTGGTGGGTGAATACCTCTCTCAACACCAACCCCTGATGTTAT	420						
Db	361	CCCAACCGGTGATGTGGTGGGTGAATACCTCTCTCAACACCAACCCCTGATGTTAT	420						
QY	421	CTCACCACCAATCACTTTGCAATTTCCGAGAAATCTCATCTTTCAGGCGCGTGTGGA	480						
Db	421	CTCACCACCAATCACTTTGCAATTTCCGAGAAATCTCATCTTTCAGGCGCGTGTGGA	480						
QY	481	GAACTACATTACAGCAGTGAAGAACATGTCTATGCGGTGTTGGAAATGATGCGGAGGG	540						
Db	481	GAACTACATTACAGCAGTGAAGAACATGTCTATGCGGTGTTGGAAATGATGCGGAGGG	540						
QY	541	GTGGGGGATAAGCAGAGGAATACGTTTACGAGGTTGCTGAAGGATGAGAAAGTGATTC	600						
Db	541	GTGGGGGATAAGCAGAGGAATACGTTTACGAGGTTGCTGAAGGATGAGAAAGTGATTC	600						
QY	601	GTGCTTCAGGTTGAACCACTTACCCGCTTGCCTGAGGTGCAAGCACTCAACCGGAATTT	660						
Db	601	GTGCTTCAGGTTGAACCACTTACCCGCTTGCCTGAGGTGCAAGCACTCAACCGGAATTT	660						
QY	661	GGTTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGCTTAAAGATCTAAACAGCAC	720						
Db	661	GGTTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGCTTAAAGATCTAAACAGCAC	720						
QY	721	ATCTGGCTTGCAAATCTGTCTACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGAC	780						
Db	721	ATCTGGCTTGCAAATCTGTCTACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGAC	780						
QY	781	TTCTTTTTTTCATCAATGTTGTGACCTCTACAGGTAATGACTAATGGGAGGTTTAAAG	840						
Db	781	TTCTTTTTTTCATCAATGTTGTGACCTCTACAGGTAATGACTAATGGGAGGTTTAAAG	840						
QY	841	TGTAAAGCATAGGTTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTGG	900						
Db	841	TGTAAAGCATAGGTTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTGG	900						
QY	901	AGGACACAGGTTGAGTGAAATATAGCAGCTTTACCTTCAGTGATGTTAAAGGAGGAG	960						
Db	901	AGGACACAGGTTGAGTGAAATATAGCAGCTTTACCTTCAGTGATGTTAAAGGAGGAG	960						
QY	961	GTGTTTGTACAAGAGTTACATGTTGTGAATACAAGAGGCTGCGTACACTTCAAGGCT	1020						
Db	961	GTGTTTGTACAAGAGTTACATGTTGTGAATACAAGAGGCTGCGTACACTTCAAGGCT	1020						
QY	1021	AGCTGATAATAGGCTTGCCTTTCCAGAAATCTGCTGCTGATTAACCAAAACACACCCCTT	1080						

Db 841 TGTAAAGCATAGGGTTTGGCGTGACACACGAAGTCAAGGTTATCAATGATCTACTTTGG 900
QY 901 AGGACAGCGTTGAGTGAATAATATAGCACCCTTTACCTTCAGTGATGTTAAAAAGGAGAGA 960
Db 901 AGGACAGCGTTGAGTGAATAATATAGCACCCTTTACCTTCAGTGATGTTAAAAAGGAGAGA 960
QY 961 GTGTTTGTACAAGAGTTTCACATGTTGTGAATACAAAGAGGCTGGGTACACTTCAAGGCT 1020
Db 961 GTGTTTGTACAAGAGTTTCACATGTTGTGAATACAAAGAGGCTGGGTACACTTCAAGGCT 1020
QY 1021 AGCTGATAATAGGCTGGCCCTTTCAGAAATCTGCTGCTGATTAACCAACACACCCCTT 1080
Db 1021 AGCTGATAATAGGCTGGCCCTTTCAGAAATCTGCTGCTGATTAACCAACACACCCCTT 1080
QY 1081 CAAATTCCTCAATTTTACGACGCTGTTATTAACCCCAATTTTCTTTCTTTCTTTTCC 1140
Db 1081 CAAATTCCTCAATTTTACGACGCTGTTATTAACCCCAATTTTCTTTCTTTCTTTTCC 1140
QY 1141 TGTGCTGTCTAGGTTTCAACAGTTGACTCTACTTGACATATATAGAAATGAATAGGT 1200
Db 1141 TGTGCTGTCTAGGTTTCAACAGTTGACTCTACTTGACATATATAGAAATGAATAGGT 1200
QY 1201 TAAAGTGTATATCAATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1260
Db 1201 TAAAGTGTATATCAATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1260
QY 1261 CCCTTTCTCAATTTGCTCAATGAACGCACTCTAGTTACAAAAAATGAAAAA 1318
Db 1261 CCCTTTCTCAATTTGCTCAATGAACGCACTCTAGTTACAAAAAATGAAAAA 1318

RESULT 5
AB181372
LOCUS AB181372 1360 bp mRNA linear PLN 09-JUN-2005
DEFINITION Vigna angularis VaGA2oxA1 mRNA for gibberellin 2-oxidase, complete cds.
ACCESSION AB181372
VERSION AB181372.1 GI:67077811
KEYWORDS Vigna angularis (adzuki bean)
SOURCE Vigna angularis
ORGANISM Vigna angularis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
REFERENCE 1
AUTHORS Park,S.; Nakajima,M., Xu,Z., Tomioka,K., Sakane,M. and Yamaguchi,I.
TITLE Gibberellin 2-oxidases from adzuki bean hypocotyl
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1360)
AUTHORS Nakajima,M., Xu,Z., Park,S., Tomioka,K., Sakane,M. and Yamaguchi,I.
TITLE Direct Submission
SUBMITTED (08-JUN-2004) Masatoshi Nakajima, The University of Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture, 1-1-1 Yayoi, Bunkyo, Tokyo, 113-8657, Japan
(E-mail:nkim@agri.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192, Fax:81-3-5841-8025)
FEATURES
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1..1360
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FGPALSSEKIAPLPSVMVGBESLYKBFTWMEYKAAVTSRLADNRLAPFEKASATD"
ORIGIN
Query Match 84.3%; Score 1110.8; DB 15; Length 1360;
Best Local Similarity 91.6%; Pred. No. 3.7e-281;
Matches 1214; Conservative 0; Mismatches 93; Indels 18; Gaps 3;
QY 10 CTTTACCCCTGTTCTGCTTCTCTTTTCATAGTAACAATCGACAAACAACAACAACCAT 69
Db 27 CTTACCCCTGTTCTGCTTCTCTTTTCATAGTAACAATCGACAAACAACAACAACCAT 84
QY 70 GGTGTTCTGCTCAGCCAGCATTTGAACAGTTTTTCTTCTGAAACCATTTCAAGTCCAC 129
Db 85 GGTGTTCTGCTCAGCCAGCATTTGAACAGTTTTTCTTCTGAAACCATTTCAAGTCCAC 144
QY 130 GCCCTTGTTCAGGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAAGATCTCAT 189
Db 145 GCCCTTGTTCAGGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAAGATCTCAT 204
QY 190 AGTGAAACCCCTGTAGGGACTTCGGCTTCTCAAGCTTGTGAACCATGTTTCCATTGGA 249
Db 205 AGTGAGGCCCTGTAGGGACTTACGGCTTCTCAAGCTGTAACCATGTTTCCATTGGA 264
QY 250 GTTAATGGCCCAATTTAGAAAAAGCGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAA 309
Db 265 GTTAGTGGCCCAATTTAGAAAAAGCGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAA 324
QY 310 AGACAGACTGGTCCCGGACCTTTTCGGCTATGTTAGCAAGAGGATTTGGCCCAACCG 369
Db 325 AGACAGGGCTGGTCCCGGACCTTTTCGGCTATGTTAGCAAGAGGATTTGGCCCAACCG 384
QY 370 TGATGTCGGTGGGTGCGAATACCTCTCTCAACACCAACCTGATGTTATCTCACCCAA 429
Db 385 CGATGTCGGTGGGTGCGAATACCTCTCTCAACACCAACCTGATGTTATCTCACCCAA 444
QY 430 ATCACTTTGCAATTTTCCGAGAAAAATTCCTCATCATTTTCAAGGCGGTGGTGGAGAACTACAT 489
Db 445 ATCACTCTCAATTTTCCGTAAGTCTCTCATCATTTTCAAGGCGGTGGTGGAGAACTACAT 504
QY 490 TACAGCAGTGAAGAACATGTTGCTATGCGGTGTTGGAATTTGATGCGGAGGGGTTGGGGAT 549
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QY 550 AAGCAGAGGAATAGTTTAAAGCAGGTTGCTGAAGGATGAGAAAGTGTCTGCTTCAG 609
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QY 610 GTTGAACCACTACCGCCCTTCCCTCAGGTGCAAGCACTGAACCCGGAATTTGGTTGGGTT 669
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QY 670 TGGGAGACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGGGCTT 729
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QY 730 GCAATCTGCTCAGATGACCTTGGGTTTTCAGTCCACCTGATCAGACTTCCTTTT 789
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QY 790 CATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCA 849
Db 805 CATCAATGTTGGTGATGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCA 864
QY 850 TAGGGTTTGGTGACACCAAGAGTCAAGGTTATCAATGATCTACTTTTGGAGGCCAGC 909

Query Match		36.8%;	Score 484.6;	DB 15;	Length 1406;
Best Local Similarity		70.4%;	Pred. No. 3.2e-116;		
Matches		677;	Conservative	0;	Mismatches 278; Indels 6; Gaps 2;
QY	118	ATTCAAGTTCACGCCCTTTGTTACGGGGATTCCTGTGTGTCGACCTCACGACCCCGATGC	177		
DB	57	ATTCCTCCACCAACTTCTACGAAGAAATCTCTGTGATTGACCTCTTCAAACTCGAGGC	116		
QY	178	CAAGAATCTCATAGTCAAGCCCTGTAGGACTTCGGCTCTTCAAGCTTGTGAACCATGG	237		
DB	117	AAACACTGAATATGTTAAGCCCTGTCAAGATTTGGAATCTTTAAGGTGATCAATCATGG	176		
QY	238	TGTTCCATTTGGAGTTAATGCCCAATTTAGAAACGAGGCCCTCAGGTTCTTTAAAAATC	297		
DB	177	TGTTCTCTTTGGAGTTCTATAACGAAGCTAGAAGTGAAGCTGTCAGGTTCTTCAATTTACC	236		
QY	298	TCNGTCCGAGAAGACAGAGCTGGTCCCGCCGACCTTTCGGGTATGGTAGCAAGAGAT	357		
DB	237	CCAACCAGAGAAGAAAAAGTTGCGCCCTGCTAAACCTTTTGGCTATGGTAAACAAGAGAAT	296		
QY	358	TGSCCCAAACGGTGATGTCGGTTGGGTGCAATACCTCTCCTCAACACCAACCCCTGATGT	417		
DB	297	TGCCAGAACGGTGATGTTGGTTGGATGAGTATCTTCTTTAACCAATCTCTGAAT	356		
QY	418	TATCTCACCCAAATCATCTTTGCAATTTCCGAGAAATCTCTCATCATTTTCAGGGCGGTGT	477		
DB	357	AGTTTACGAGAAAGCCGT---CACCATCCCGCGGATTCAGAATCTTTCTGGTCTTGTGT	413		
QY	478	GGAGAATCATATACAGCATGTAAGAAACATGTGCTATGCGGTGTGGAATTAATGCGCGA	537		
DB	414	GAATGACTATGTGTCAGCCGTGAGAAAGTATGGCTTGTGATGTTCTGGACATGATTCAGA	473		
QY	538	GGGTTTGGGGATAAGCAGAGGAATACGTTTACGAGGTTGCTGAAGGATGAGAAAGTCA	597		
DB	474	TGACTGAAGATTGGGCCAAGGAATGTGCTGAGCAGCTTTTAAAGATGAGAAAGCGCA	533		
QY	598	TTCTGCTCTTCAGGTTGAACACTATACCGCGCTTCCCTCGAGGTGCAAGCACTGA---ACCG	654		
DB	534	CGCTGTCTTCAGGCTAAACCACTATCCACCATGTCAGAGCTTCAAGCATTGAGTGTGCG	593		
QY	655	GAATTTGGTTGGTTGGGGAGACACAGACCCACAGATAAATTTCTGTCTTGAATCTTAA	714		
DB	594	AAATTTGATTGGGTTCCGGAGAACACACAGATCTCTCAATAATATCTGTTGTGAGATCTAA	653		
QY	715	CAGCATCTGGCTTCCAAATCTGTCTCACAGATGACCTTGGGTTTTCAGTCCCACTCA	774		
DB	654	CAACATCAGGCTGCAATCTCTCTGAAAGATGGGACATGGGTTTCAGTCCCTCCTGA	713		
QY	775	TCAGACTTCCTTTTTCATCAATGTTGGTGACCGCTCTACAGGTAATGACTAATGGGAGTT	834		
DB	714	TCAGTACTCTTTTTCATTAATGTTGGTGATTCCTTGCAGGTAATGACTAATGGGAGATT	773		
QY	835	TAAAAGTGTAAAGCATAGGTTTTTGGCTGACACACAAAGTCAGGTTATCAATGATCTA	894		
DB	774	TAGGAGTGTAAAGCATAGAGTTTTTCTGACCGCTTTGAAAGTCAGGGTATCCATGATCTA	833		
QY	895	CTTTGGAGGACCGCTTCAGTGAAATATAGCACCTTTTACCTTTCAGTGTGTTAAAGG	954		
DB	834	CCTAGAGGACCACTTTTGAATGAAAGATAGCCCCCTTTATCTCTACTAATGGAGGAGG	893		
QY	955	AGAGGAGTGTTTGTACAAAGAGTTTCATGTTGTGTAATACAAAGGCTGCGTACATCTTC	1014		
DB	894	TGAGAAAGTTTGTATAGGAATTCACATGGTGTGTAATACAGAACTCAGCTTACAGAC	953		
QY	1015	AGGGTAGCTGATAATAGGCTTGCCCTTTTCAGAAATCTGCTGTGATTAACCAACAC	1074		
DB	954	GAGGCTTGGTGACACAGGCTCAAAATCTTTTGAGAAATCTGTAGGCCAGTGATTTAAC	1013		
QY	1075	A 1075			
DB	1014	A 1014			

RESULT 9
AY594292
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL

FEATURES
Source

CDS

ORIGIN

Query Match 35.2%; Score 464.4; DB 15; Length 1245;
Best Local Similarity 67.9%; Pred. No. 6.6e-111;
Matches 680; Conservative 0; Mismatches 316; Indels 6; Gaps 2;

QY	68	ATGGTGTGTTCTCTCTCAGCCAGCATTTGAACCAAGTTTTTCTCTCTGAAACCATTTCAAGTCC	127
DB	1	ATGGTGTGTTCTCTCTCAAAACCAAGCAATGGAACAGTTCTGCTTAGTCAAGAACTGTAAGCT	60
QY	128	AGCCCTTGTTCACGGGGATTCCTGTGTGACCTTCAGCACCCCGATGCCAAGATCTC	187
DB	61	CCACATTAATCCCGGGTGTTCATTTGATAGACCTCTCGAAACCTGACTCGAAACACCTC	120
QY	188	ATAGTGAACGCGCTGTAGGACTTCGCGTCTTCAAGCTTGTCAACCATGTTGTTCATTG	247
DB	121	CTTGTTAAGGCTCTCAAGAGTTTGGATTTTCAAGTCAATTAATCACGGTGTTCACAC	180
QY	248	GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	307
DB	181	GAATTCATCACCAACTTGAGTCTGAGCTGTCAAATCTTCTCTTTGCCCTTTCCGAT	240
QY	308	AAAGCAGAGCTGTGTCCTCCCGACCCCTTTCGGCTATGTTAGCAGAGGATTTGGCCCAAC	367
DB	241	AAAGAAAACGACGAGGCCCTCTGACCCCTTTGGCTATGGTAAACAAGAGATTGGACCCAAT	300
QY	368	GGTGTATGTCGGTGTGTCGAATACCTCTCTCAACACCAACCTCTGATGTTATCTCACCC	427
DB	301	GGCGATATCGGATGGGTGGAATACATCATTCATCCACCAATTCGGAATTCGAATACCAA	360
QY	428	AAATCATTGTGATTTTCCGAGAAAATCTCATCATTTTCAGGGCGGTGGTGAGAACTAC	487


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Qy 488 ATTACAGCAGTGAAGAACATGCTATGCGGTGTGGAAATTCATGCGGAGGGTTGGG 547
Db 421 GTATCATCATAGTAAGAAATGCTGTGTAATCTGTAATTAATGCGAGAGTTTGAT 480
Qy 548 ATAAGCAGAGGAATACTGTTAAGCAGGTTGCTGAAAGGATGAGAAAAGTGAATTCGTGCTTC 607
Db 481 ATTACGCCAAAGAACGTTTACAGCAAGCTCTTGATGATGAACAGAGTGAATCTGTTTC 540
Qy 608 AGTTGAACCACTACCCGCTTCCCTGAGTGCAGCACTGAA---CGGAAATTTGGTT 564
Db 541 AGACTCAATCACTACCCCTATCTGACCTTCAAGAACTCATGCGCAGGAAATTAAT 600
Qy 665 GGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTTAAGATCTAAGCAGCATCT 724
Db 601 GGTTTGGAGAACACACTGACCCACCAATCATCTCTGTTTAAGATCAAAACACTTCT 560
Qy 725 GCGTTGCAATCTGTCTACAGATGCACTTGGGTTTCAGTCCCACTGATCAGACTTCC 784
Db 661 GCGCTTCAATACAAATGGAAGATGAAGCTGGATATCCATTTCCACCTGATCAGAGTTCA 720
Qy 785 TTTTTCATCAATGTTGGTGCACCTCTACAGGTAATGACTAATGGAGGTTTAAAGTGA 844
Db 721 TTTCTTATCAATGTTGGTGACTCAACGCGAGGTTTGAACAAATGGGAGGTTTAAAGTGA 780
Qy 845 AAGCATAGGTTTGGCTGACACACGAAGTCAAGGTTATCAATGATCTACATTTTCGAGGA 904
Db 781 AAGCATAGGTTTGGCAACAGTATGAATCAAGCTTTCGATGATTTATTTTCGAGGA 840
Qy 905 CCAGCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAGGAGAGGAGTGT 964
Db 841 CCACCGTTGAGTGAAGATAGCTCCATTTGCCATCACTTATG---GAAGTGAAGACAGC 897
Qy 965 TTGTCAAAAGAGTTCACTGGTGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCT 1024
Db 898 TTGTCAAAAGAGTTTACATGGTTGAGTACAAAAGTCTGCATACAAGTCAAGACTAGCT 957
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Db 958 GATAACAGACTGGTCTGTTGAGAAAAATTCGTCCTCATAA 999

RESULT 10
CWA315663
LOCUS CWA315663
DEFINITION Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox gene).
ACCESSION AJ315663
VERSION AJ315663.1 GI:32127336
KEYWORDS ga2ox gene; gibberellin 2-oxidase.
SOURCE Cucurbita maxima (winter squash)
ORGANISM Cucurbita maxima
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
REFERENCE 1
AUTHORS Frisse,A. and Lange,T.
TITLE Gibberellin biosynthesis in young seedlings of Cucurbita maxima L
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1383)
AUTHORS Lange,T.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2001) Lange T., Botanical Institute, TU Braunschweig, Mendelssohnstr. 4, D-38106 Braunschweig, GERMANY
COMMENT related entry AJ315662.
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ORIGIN

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Query Match 35.1%; Score 462.2; DB 15; Length 1383;
Best Local Similarity 68.7%; Pred. No. 2.5e-110;
Matches 651; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

Qy 125 TCCAGCCCTTGTTCACGGGATTCCTGTGTGACCTCAGCACCACCAGAT 184
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Qy 185 CTCATAGTGAAGCGCTGTAGGACCTTCGCTTCTTCAAGCTTGTGAACCATGTTTCCA 244
Db 124 CTCATGTCAAGCTTGTGAAGAACTCGGATTCCTTAAAGTTGTCAACATGGTGTCCCC 183
Qy 245 TTGGAGTTAATGGCCAAATTTAGAAAAAGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304
Db 184 ATGGATTAATCTCTCTCTTGAATCAGATCCACCAATTTCTTCCCTTCCCTCTCT 243
Qy 305 GAGAAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGTGAGCAAGAGGATTTGCCCA 364
Db 244 GAAAAACAGAGAGCTGGCCCTCTCTTCCCTTTTGGCTATGGAACAAACAAATTTGCCCGC 303
Qy 365 AACGTTGATGTCGGTGGTTCGAATACCTCTCCTCCCAACACCAACCTGATGTTATCTCA 424
Db 304 AATGGCGATGTGGTGGTGGATATCTCTCTTCTTGAACACTCATCTCGAATCCAACTCC 363
Qy 425 CCCAAATCACTTTTTCGAGAAAAATCCTCATCATTTTCAGGGCGGTGGTGAAGAAC 484
Db 364 GATGGGTTCTCTCATTTTCGGCCCAAGACCCACAAAAAATCTCGCTCTCTGTGAACGAT 423
Qy 485 TACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAAATTTGATGCGGAGGGGTTG 544
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Qy	245	TTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAANAATCTCAGTCC	304
Db	228	ATGGAAATTAATCTCTCTCTTGAATCAGAATCACCACAAATTTCTTCTCCCTTCCCTCTCT	287
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Qy	365	AACGGTGAATCGGTTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTATCTCA	424
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Db	408	GATGGGTTTCTCTCCATGTTTGGCCAAAGCCACAAAACTCCGCTCTGCTGTGAACGAT	467
Qy	485	TACATTTACAGCACTGAAGAACAATGTGCTATGCGGTGTGGAAATGATGGCGGAGGGTTG	544
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Db	828	GTGAAGCATAGGGTTTTGACAAACAGCTCGAAGCTCAAGGGTTTCAATGATCTACTTCGGT	887
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Db	1008	GCTGACAAACAGGCTTGTGGCCCTTTGAAAGAAATTCAGCCTCATAATC	1054
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AB125232			
LOCUS			
DEFINITION			
AB125232.1			
KEYWORDS			
SOURCE			
ORGANISM			
Nicotiana tabacum (common tobacco)			
AB125232			
AB125232.1			
GI:46849528			
1292 bp			
mRNA			
linear			
PLN 29-APR-2004			
Nicotiana tabacum GA2ox1 mRNA for gibberellin 2-oxidase 1, complete cds.			

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Sakane, M., Nakajima, M. and Yamaguchi, I.
Molecular cloning of GA 2-oxidase in BY-2
Unpublished
2 (bases 1 to 1292)
Sakane, M., Nakajima, M. and Yamaguchi, I.
Direct Submission
Submitted (28-OCT-2003) Masayuki Sakane, University of Tokyo,
Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo
113-0032, Japan [E-mail: m-sakane@grl.ch.a.u-tokyo.ac.jp,
URL: http://pgrl.ch.a.u-tokyo.ac.jp/, Tel: 81-3-5841-5158 (ex. 25158),
Fax: 81-3-5841-8025]

FEATURES

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ORIGIN

Query Match

Best Local Similarity 65.7%; Pred. No. 6.e-108;

Matches 692; Conservative 0; Mismatches 355; Indels 6; Gaps 2;

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DB 128 CAATATCTCATCTTCAATGGTTCATGATGACCTCTCTAAACCTAACTCTTAA 187

QY 181 GAATCTCATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT 240

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DB 308 TTCTGAGAAACAAAAGCTGGGCCAGCTGATCTCTTTTGGCTATGGAACAAGAAATTGG 367

QY 361 CCCAAACGGTGTGTGGTGGGTGCAATACCTCTCTCAACACCAACCTCGATGTTAT 420

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MMY09113

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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JOURNAL

PUBMED

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	VERSION			AR452821.1													
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	KEYWORDS																
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	ORGANISM			Unknown.													
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Miao, G.-H., Famodu, O.O., Lee, J.-M., Lohman, K.N., Rendina, A.R.,		115			ACATTCAAGTCCAGCCCTTGTTCAGGGGATTCTGTGGTCGACCTCAGCACCACCGGA				174								
Sakai, H., Wang, Z., Caimi, P.G., Fang, Y., Shen, J.B.J., Zoughi, I.L.,		206			GAACGTGCATGCCAACCAAAATTTCTCTCAACAATCCCATAGTGGACCTCTCCAAACCTGA						265						
Anderson, S.L., Shi, J., Lu, G., Helentjaris, T.G. and Li, C.P.		175			TGCCAAAGATCTCATAGTGAACGCCCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCA							234					
Plant metabolism genes		266			TCAAAAGACCTTTATAGTGAAGCCTTTGTGAGAGTTTGGATTCTTCAAGTCATCATCA								325				
Patent: US 6677502-A 13 13-JAN-2004;		235			TGGTGTTCATTTGGAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAA									294			
E.I. du Pont de Nemours and Company and Pioneer Hi-Bred		326			TGGTGTCTCATGGAAGCTATATCCGAATTGGAATATGAAGCCTTCAAATTTCTTCTCTAT										385		
International, Wilmington, DE		295			ATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCGACCTTTCGGCTATGTTAGTAGCAGAG											354	
Location/Qualifiers		386			GTCACCTCAATGAAGGAAAAGTAGGACCTCCCAATCCATTGGGTATGGTAGCAAGAA												445
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		475		GGTGGAGACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTTGGAAATTTGATGGC						534							
		554		GTTGAACAGTTATGCTCTTCTGTGTGAGGAAGATGGCATGTGAGATTCTTGTAGTTGATGGC							613						
</																	

535	QY	GGAGCGGTTGGGGATAAGCGCAGAGGAATACGTTAAGCAGAGGTTGCTGAAGCATGAGAAAG	594
614	Db	AGAGGGGTTGAAGATTACAGCAAAAGGATGTGTTTAGCAAGCTTCTAATGGATAACAAAG	673
595	QY	TGATTCTGCTTCAGGTTTGAAACCACTACCGCCTTGGCCTTGAGGTGCAAGCATGCAACCG	654
674	Db	TGACTCTATTTTCAGGGTGGAATCAATACCCCTGTGCTTGAATGACTCTGAATGATCA	733
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794	Db	CAACACTTCAGGCCCTTCAGATTTATCTTAGAGATGGAAATTGGATTTTCAGTCCCAACAGA	853
775	QY	TCAGACTTCCTTTTTCATCAATGTTGGTGAGCGCTCTACAGGTATATGACTAATGGGAGGTT	834
854	Db	TGACAAATCCCTTTTATTAAACGTTGGTGATTTCTCTTCAGGTTATATGACAAATGGAAGGTT	913
835	QY	TAAAGGTATAAGCATAGGTTTTGGCTGTGACACACCAAGCTCAAGGTTATCAATGATCTA	894
914	Db	CCGAAGTGTGAGACACAGAGGTTTGGCAATATGGGTTCAAGTCCAGGCTTTCAATGATTTA	973
895	QY	CTTTGGAGGACACAGCGTTTGAGTGAATAATAGACACCTTTACCTTCAGTGTGTTTAAAAGG	954
974	Db	CTTTGGAGGTCCACTTTGAGTGAGAAATATAGCAACATATCTCTCTCTATG---AANGG	1030
955	QY	AGAGGAGTGTTTGTATCAAAAGAGTTTCACATGGTGTGAATACAAAGAGCGTCGTACACTTC	1014
1031	Db	AAAAGAAAGCTATATAAGAGTTTACCTGCTTTGAGTACAAAAATCAATCTACGGTTC	1090
1015	QY	AAGGCTAGCTGATATATAGGCTTGCCCTTTCCAGAAATCTGCTGCTGATTA	1066
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RESULT 15
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 LOCUS linear 1365 bp DNA PAT 20-FEB-2004
 DEFINITION Sequence 5 from patent US 6677502.
 ACCESSION AR452817
 VERSION AR452817.1 GI:42684843
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1365)
 AUTHORS Allen,S.M., Kinney,A.J., Rafalski,J.A., Orozco,E.M. Jr.,
 Miao,G.-H., Fancodu,O.O., Lee,J.-M., Lohman,K.N., Rendina,A.R.,
 Sakai,H., Weng,Z., Cai,M.P.G., Fang,Y., Shen,J.B.J., Zoughi,I.L.,
 Anderson,S.L., Shi,J., Lu,G., Helentjaris,T.G. and Li,C.P.
 TITLE Plant metabolism genes
 JOURNAL Patent: US 6677502-A 5 13-JAN-2004;
 E.I. du Pont de Nemours and Company and Pioneer Hi-Bred
 International; Wilmington, DE
 FEATURES
 source Location/Qualifiers
 1..1365
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN

	Query Match	32.6%	Score 429.2	DB 6	Length 1365
	Best Local Similarity	65.6%	Pred. No. 1.2e-101		
	Matches 664	Conservative 0	Mismatches 333	Indels 15	Gaps 2
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Db	153	AACAACAAGAAAATGTTGTTGTTCCAAAGCAACAACAAGCAATCTCTACATTA	212		
Qy	115	ACATTCAAGTCACGGCCCTTGTTCACGGGGATTCCTGTGTCAGCACTCAGGACCCCGA	174		
Db	213	GAACGTGATGCAACCAAAATTTTCTCAACAATTCAGATGTGACCTCTCCAAACCTGA	272		

Search completed: December 27, 2005, 21:42:41
Job time : 7019.33 secs

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273	Db	TG	CA	AA	GA	G	C	C	T	T	A	T	A	G	T	G	A	A	G	G	C	T	T	G	T	G	A	A	G	C	T	T	A	T	A	G	A	G	C	T	T	C	A	A	G	T	C	A	A	T	C	A		332	
235	QY	TG	GT	G	T	T	C	C	A	T	T	A	T	G	C	C	A	A	T	T	A	G	A	A	C	G	A	A	C	G	C	C	T	C	A	G	G	T	T	C	T	T	T	A	A	A	A		294						
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595	QY	T	G	A	T	C	G	T	C	T	C	A	G	T	T	G	A	A	C	A	C	T	A	C	C	G	C	C	T	T	G	C	C	T	G	A	G	G	T	C	A	A	C	A	C	T	G	A	A	C	C	G		654	
681	Db	T	G	A	C	T	A</																																																

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 16:12:28 ; Search time 888.539 Seconds
(without alignments)
9885.961 Million cell updates/sec

Title: US-10-670-454-1

Perfect score: 1318

Sequence: 1 gtttctctcttaccctgt.....caaaaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:.*
1: Geneseqn1990s:.*
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3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
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9: Geneseqn2003bs:.*
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11: Geneseqn2003ds:.*
12: Geneseqn2004as:.*
13: Geneseqn2004bs:.*
14: Geneseqn2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1318	100.0	1318	3	Aaz55912 Runner be
2	999	75.8	999	13	Adt62692 DNA encod
3	893.8	67.8	1359	3	Aaz99471 Soybean g
4	893.8	67.8	1359	6	Aad40261 Soybean G
5	430.8	32.7	1352	12	Adm94213 Soybean D
6	429.2	32.6	1365	12	Adm94205 Soybean D
7	425.8	32.3	1237	3	Aaz55916 Arabidops
8	425.4	32.3	1026	6	Abz13545 Arabidops
9	425.4	32.3	1026	8	Ada67975 Arabidops
10	424.8	32.2	1403	3	Aaz99472 Soybean g
11	424.8	32.2	1403	6	Aad40262 Soybean G
12	382.8	29.0	1008	3	Aaz55917 Soybean G
13	363.6	27.6	1473	12	Adm94207 Wheat Dio
14	356.6	27.1	1224	3	Aac39277 Arabidops
15	356.6	27.1	1316	3	Aaz55915 Arabidops
16	355.6	27.0	1851	14	Aeb67733 Rice geno
17	354	26.9	984	8	Ada70120 Rice gene
18	354	26.9	984	12	Adk00081 Rice cdna
19	354	26.9	1271	14	Aeb67784 Rice geno

20	354	26.9	1650	12	ADM94203	Adm94203 Rice Diox
21	315.8	24.0	1555	12	ADM94201	Adm94201 Corn Diox
22	311	23.6	783	3	Aaz99474	Aaz99474 Cotton gi
23	311	23.6	783	6	AAD40264	Aad40264 Cotton GA
24	302.8	23.0	831	13	ADx11608	Adx11608 Plant ful
25	285	21.6	927	12	ADI45210	Adi45210 Rice isop
26	273.8	20.8	860	13	ADx13286	Adx13286 Plant ful
27	188.6	14.3	1322	13	ADx09682	Adx09682 Plant ful
28	187.2	14.2	1065	8	ADA69812	Ada69812 Rice gene
29	172.2	13.1	919	13	ADx63586	Adx63586 Plant ful
30	166	12.6	811	3	Aaz99478	Aaz99478 Maize gib
31	166	12.6	811	6	AAD40268	Aad40268 Maize gib
32	161.8	12.3	95769	8	ADA68659	Ada68659 Arabidops
33	156.2	11.9	504	12	ADI45683	Adi45683 Corn isop
34	155.6	11.8	403	3	Aaz99473	Aaz99473 Soybean g
35	155.6	11.8	403	6	AAD40263	Aad40263 Soybean G
36	154.8	11.7	406	3	Aaz99475	Aaz99475 Cotton gi
37	154.8	11.7	406	6	AAD40265	Aad40265 Cotton GA
38	152.4	11.6	966	3	Aaz99469	Aaz99469 Arabidops
39	152.4	11.6	966	6	AAD40259	Aad40259 A. thalia
40	150.4	11.4	537	12	ADI45522	Adi45522 Banana is
41	141	10.7	480	3	AAC50271	Aac50271 Arabidops
42	135.2	10.3	683	3	AAC54605	Aac54605 Arabidops
43	133.6	10.1	687	3	AAC53074	Aac53074 Arabidops
44	120	9.1	426	3	Aaz99477	Aaz99477 Maize gib
45	120	9.1	426	6	AAD40267	Aad40267 Maize GA

ALIGNMENTS

RESULT 1		AAZ55912		AAZ55912 standard; CDNA; 1318 BP.	
XX	ID	AAZ55912	standard; CDNA; 1318 BP.		
XX	AC	AAZ55912;			
XX	DT	10-APR-2000	(first entry)		
XX	DE	Runner bean gibberellin 2-oxidase PCGA2ox1 cDNA.			
XX	KW	Gibberellin 2-oxidase; PCGA2ox1; runner bean; 2-beta-hydroxylation;			
XX	KX	inactivation; growth inhibition; ss.			
XX	OS	Phaseolus coccineus.			
XX	FT	Key	Location/Qualifiers		
FT	CDS	68..1086	/*tag= a		
FT		/product= "Gibberellin 2-oxidase PCGA2ox1"			
FT		/transl_except= (pos:1058..1063, aa:Ala)			
XX	PN	WO9966029-A2.			
XX	PD	23-DEC-1999.			
XX	PP	11-JUN-1999;	99WO-GB001857.		
XX	PR	12-JUN-1998;	98GB-00012821.		
XX	PR	15-JUL-1998;	98GB-00015404.		
XX		(UYBR-) UNIV BRISTOL.			
XX	PI	Thomas SG, Hedden P, Phillips AL;			
XX	DR	WPI; 2000-097742/08.			
XX	DR	P-PSDB; AAY58597.			
XX	PT	New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.			
XX	PS	Claim 1; Fig 1; 42pp; English.			

XX CC This sequence represents cDNA encoding a runner bean gibberellin (GA) 2-
CC oxidase, PGGA2ox1. This enzyme is a GA 2-beta-hydroxylase that acts on
CC C19-GAs and for which 2-beta-hydroxylation is its only activity.
CC Hydroxylation at the 2-beta position of a GA results in a biologically
CC inactive product, and is the most important route for GA metabolism in
CC plants, ensuring that the active hormones do not accumulate in plant
CC tissues. The nucleic acids can be used to transform plants so that
CC gibberellin 2-oxidase can be constitutively over-expressed or otherwise
CC enhanced to reduce the concentration of bioactive GAs in the plants and
CC therefore to inhibit plant growth. Growth inhibition is useful in many
CC agricultural and horticultural applications such as enhancing lodging-
CC resistance and grain yield in cereals, improving seedling quality,
CC reducing the growth of amenity grasses, reducing shoot growth in orchard
CC and ornamental trees, improving tolerance to cold, drought and infection,
CC and increasing yields (by the diversion of assimilates from vegetative to
CC reproductive organs). The nucleic acids may also be used to induce male
CC and/or female sterility (by expression in floral organs), prevent pre-
CC harvest sprouting, reduce shoot growth in hedging plants, inhibit
CC reversionability in the development or germination of seeds and reduce shoot
CC growth in commercial wood species. Antisense constructs of the nucleic
CC acids can also be used to transform plants to reduce the expression of GA
CC 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set
CC and growth in seedless grapes, citrus fruits and pears), improve skin
CC texture and fruit shape in apples, increase stem length and therefore
CC yield in sugar cane, increase yield and earliness in celery and rhubarb,
CC improve matting yields and quality in cereals (particularly barley), and
CC increase growth in woody species

Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1318;	DB 3;	Length 1318;
Best Local Similarity	100.0%;	Pred. No. 0;		
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Qy	1	GTGTTCTCTTCTCTACCCCTGTTCTGCTTCTCTTTTTTCATAGTAACAATCGCAACAACAAC	60	
Db	1	GTGTTCTCTTCTTACCCCTGTTCTGCTTCTCTTTTTTCATAGTAACAATCGCAACAACAAC	60	
Qy	61	AACAACCATGGTTGTTCTGCTCTACGCGAGCATTGAAACAGTTTTTCTTCTGAAACCAT	120	
Db	61	AACAACCATGGTTGTTCTGCTCTACGCGAGCATTGAAACAGTTTTTCTTCTGAAACCAT	120	
Qy	121	CAAGTCCACGCCCTTGTTGTCACGGGGATTCTGTGTCGACCTCACGCAACCCCGATGCCAA	180	
Db	121	CAAGTCCACGCCCTTGTTGTCACGGGGATTCTGTGTCGACCTCACGCAACCCCGATGCCAA	180	
Qy	181	GAATCTCATAGTGAACGCCCTGTAGGGACTTCGGCTTTCTTCAAGCTTGTGAACCAATGGTG	240	
Db	181	GAATCTCATAGTGAACGCCCTGTAGGGACTTCGGCTTTCTTCAAGCTTGTGAACCAATGGTG	240	
Qy	241	TCCATTGCGAGTTAATGCGCCAAATTTAGAAAAACGAGCGCCCTCAGGTTCCTTAAAAAATCTCA	300	
Db	241	TCCATTGCGAGTTAATGCGCCAAATTTAGAAAAACGAGCGCCCTCAGGTTCCTTAAAAAATCTCA	300	
Qy	301	GTCCGAAAAACAGAGACTGGTCCCCCGACCCCTTTCGGCTATGGTAGCAAGAGGATTTGG	360	
Db	301	GTCCGAAAAACAGAGACTGGTCCCCCGACCCCTTTCGGCTATGGTAGCAAGAGGATTTGG	360	
Qy	361	CCCAACCGGTGATGTCGGTTGGGTCGAATACCTCCTCTCAACACCAACCCCTGATGTTAT	420	
Db	361	CCCAACCGGTGATGTCGGTTGGGTCGAATACCTCCTCTCAACACCAACCCCTGATGTTAT	420	
Qy	421	CTCACCCAAATCACTTTGCAATTTTCCGAGAAAAATCCTCATCATTTACGGGCGGTGGGA	480	
Db	421	CTCACCCAAATCACTTTGCAATTTTCCGAGAAAAATCCTCATCATTTACGGGCGGTGGGA	480	
Qy	481	GAACACATTTACAGCAGTGAGACATGCTGATGCGGTGTTGGAATTTGATGGCGGAGGG	540	
Db	481	GAACACATTTACAGCAGTGAGACATGCTGATGCGGTGTTGGAATTTGATGGCGGAGGG	540	
Qy	541	GTGTTGGGATTAAGGCAGAGGAATACGTTTAAGCAGGTTGCTCAAGGATCAGAAAACTGATTC	600	

RESULT 2

RESOLUTION
ADT62692

ADT62692
ID ADT62692 standard; DNA; 999 BP.

XX
26070104 DT

AC ADT62692;

XX
12070104

DT 13-JAN-20

[illegible]

DE DNA encoding Phaseolus coccineus gibberellin 2-oxidase.

XX

KW DNA plasmid; transfe

KW expression cassette;

KW gibberellin

XX

50

PR 09-APR-2003; 2003US-0461459P.
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 PI Gilbertson L, Krieger E, Zhang W, Ye X;
 XX WPI; 2004-758349/74.
 DR
 XX
 XX New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
 PT first border region linked to a transgene linked to an Agrobacterium Ti
 PT plasmid second border region, useful for enhancing production of
 PT transgenic plants.
 XX
 XX Example 1; SEQ ID NO 3; 77bp; English.
 PS
 XX The present invention relates to a DNA plasmid comprising a transfer DNA
 CC (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
 CC to at least one transgene linked to an Agrobacterium Ti plasmid second
 CC border region, and located in the DNA plasmid outside of the T-DNA is a
 CC plant expression cassette comprising a plant cell non-lethal negative
 CC selectable marker gene linked to a vector backbone DNA. Also disclosed
 CC are a method for enhancing the selection of transgenic plants that do not
 CC contain vector backbone DNA, a method for reducing the copy number of a
 CC transgene in a plant cell, and a transgenic plant produced by the method.
 CC The DNA plasmid comprises the expression cassette comprising a promoter
 CC that functions in plant cells operably linked to a plant cell non-lethal
 CC negative selection marker gene. The promoter is a constitutive promoter.
 CC The promoter expresses the linked non-lethal negative selection marker
 CC gene product in tissue culture during plant regeneration. The plant cell
 CC non-lethal negative selectable marker gene comprises a plant hormone
 CC biosynthetic pathway gene, degradative gene, biosynthetic interference
 CC substrate-diverting gene or signalling gene, or metabolic interference
 CC gene. The transgene is a plant positive selectable marker gene selected
 CC from antibiotic resistance and herbicide resistance. The transgene
 CC comprises a transgene of agronomic interest. The plant hormone
 CC biosynthetic pathway gene is selected from gibberellic acid pathway
 CC genes, cytokinin pathway genes, auxin pathway genes, ethylene pathway
 CC genes, and abscisic acid pathway genes. The plasmid is useful for
 CC enhancing the production of commercially viable transgenic plants. The
 CC present sequence represents DNA encoding Phaseolus coccineus gibberellin
 CC 2-oxidase. The sequence is used as a non-lethal negative selectable
 CC marker gene.
 XX
 SQ Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

QY 428 AAATCATTTCATTTTCCGAGAAAAATCCTCATCATTTTCAGGCGGTGGTGAGAACTAC 487
 DB 361 AAATCATTTCATTTTCCGAGAAAAATCCTCATCATTTTCAGGCGGTGGTGAGAACTAC 420
 QY 488 ATTACAGCAGTGAAGACATCTGTATGCGGTGTTGGAAATGATGCGCGAGGGTTGGG 547
 DB 421 ATTACAGCAGTGAAGACATCTGTATGCGGTGTTGGAAATGATGCGCGAGGGTTGGG 480
 QY 548 ATAAGGCGAGAGGAATACCTTAAGCAGAGTTGCTGAAGGATGAGAAAAGTATTTCGCTTC 607
 DB 481 ATAAGGCGAGAGGAATACCTTAAGCAGAGTTGCTGAAGGATGAGAAAAGTATTTCGCTTC 540
 QY 608 AGGTTGAACCACTACCCCGCTTGCCTGAGTGCAGCACTGAACCGGAATTTGGTTGGG 667
 DB 541 AGGTTGAACCACTACCCCGCTTGCCTGAGTGCAGCACTGAACCGGAATTTGGTTGGG 600
 QY 668 TTTGGGAGCAGACAGACCCACAGATAATTTCTGTTAAAGATCTAAACAGCACATCTGC 727
 DB 601 TTTGGGAGCAGACAGACCCACAGATAATTTCTGTTAAAGATCTAAACAGCACATCTGC 660
 QY 728 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTTT 787
 DB 661 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTTT 720
 QY 788 TTCAATCAATGTTGGTGACGCTCTACAGTAATGACTAATGGAGGTTTAAAGTGTAAAG 847
 DB 721 TTCAATCAATGTTGGTGACGCTCTACAGTAATGACTAATGGAGGTTTAAAGTGTAAAG 780
 QY 848 CATAGGTTTGGCTGACACAAACGAGTCAAGTTTATCAATGATCTACTTTGGAGGACCA 907
 DB 781 CATAGGTTTGGCTGACACAAACGAGTCAAGTTTATCAATGATCTACTTTGGAGGACCA 840
 QY 908 CGGTTGAGTGAATAATATAGCACTTTACCTTCAGTGTATGTTTAAAGAGGAGGAGTGTG 967
 DB 841 CGGTTGAGTGAATAATATAGCACTTTACCTTCAGTGTATGTTTAAAGAGGAGGAGTGTG 900
 QY 968 TACAAAGAGTTTCAATGTTGTAATATCAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
 DB 901 TACAAAGAGTTTCAATGTTGTAATATCAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
 QY 1028 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGATTAA 1066
 DB 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGATTAA 999

RESULT 3
 AAZ99471
 ID AAZ99471 standard; cDNA; 1359 BP.
 XX
 AC AAZ99471;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Soybean gibberellic acid 2-oxidase 1 cDNA sequence.
 XX
 KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; as.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 102..1103
 FT /*tag= a
 FT /product= "gibberellic acid 2-oxidase 1"
 FT /trans_except= (pos: 633..635, aa: Xaa)
 FT /note= "Xaa is an unspecified amino acid"
 XX
 FN WO200009722-A2.
 XX
 PD 24-FEB-2000.
 XX

/note= "Xaa = any amino acid"

US2002053095-A1.

02-MAY-2002.

10-AUG-1999; 99US-00371307.

10-AUG-1999; 99US-00371307.

(BROW/) BROWN S M.

Brown SM, Elich TD, Heck GR, Kishore GM, Logusch BW, Logusch SJ;

Piller KJ, Rao S, Ream JE;

WPI; 2002-489107/52.

P-PSDB; AAE24921.

Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.

Claim 45; Page 92-93; 155pp; English.

The invention relates to control of gibberellin (GA) levels in plants. The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase 1 cDNA

Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;

Query Match 67.8%; Score 893.8; DB 6; Length 1359;

Best Local Similarity 84.9%; Pred. No. 3.5e-237;

Matches 1069; Conservative 1; Mismatches 158; Indels 31; Gaps 5;

65 ACCATGGTGTCTCTCAGCAGCAATGAACCACTTTTCTTCTGAAACATTCAG 124

99 ACCATGGTGTCTCTCAGCAGCAATGAACCACTTTTCTTCTGAAACATTCAG 158

125 TCCAGCCCTTGTTCACGGGGATTCCTGTGGTGCACCTCAGCAGCCCGATGCCAAGAT 184

159 CCACGCCCTTGTTCGGGGATTCCTGTGGTGCACCTCAGCAGCCCGATGCCAAGAT 218

185 CTCATAGTGAACGCCCTGTAGGACATTCGGCTTTCTTCAAGCTTGTGAACCATGTGTC 244

219 CACATAGTCAATGCTCGCAGGACATTCGGCTTTCTTCAAGCTGTAACCACTGTCG 278

245 TTGGAGTTAATGGCCATTTAGAAACAGAGGCCCTCAGGTTCTTTAAATAATCTCAGTCC 304

279 TTACAGTTTCATGGCCAAATTTGGAAACAGAAACCCCTCGGGTTCTTCAAAACATTC 338

305 GAGAAAGACAGAGCTGGTCCCGCCAGCTTTGGCTATGGTAGCAGAGGATTTGGCCCA 364

339 GAGAAAGACAGAGCTGGTCCCGCTGACCTTTGGCTACGCGACGAGGATTTGGCCCT 398

365 AACGGTGTATCGGTGGTTCGAATACCTCTCTCAACCAACCAACCTCATGTATCTCA 424

399 AACGGCGATGTGGTGGTTCGAATACCTCTCTCAACCAACCAACCTCATGTATCTCC 458

425 CCCAATATCATTTGCAATTTTCGAGAAATCTCATCATTTACGGCGGTGGTGAGAAC 484

459 CCCAAGTCAAGTTCATTTTCAGAGAAAGGTCTCTCAGAAATTTACGGCGGTGGTGAG 518

QY	485	TACATTACAGCAGTGAAGAAACATGTGCTATGCGGTGTTGGAAATGATGCGGAGGGTTG	544
DB	519	TACATTAGAGCGGTGAAGAAACATGTGCTATGAGGTGTTGGAATTCATGCGTGGGATTTG	578
QY	545	GGGATAAGCGCAGAGCAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGCATTCGTC	604
DB	579	GGGATAAGCGCAGAGCAATGTTGTAGTAGGTTGCTGAAGGATGAGAAAGTGCATTCGTC	638
QY	605	TTTCCAGTTGAACCACTACCGCTTGGCTGAGGTGCAAGCACTGAAC---CGGAATTTG	661
DB	639	TTTCCAGTTGAACCACTACCGCTTGGCTGAGGTGCAAGCACTGAACCGAAGGATTTG	698
QY	662	GTTCGGTTTGGGAGCACAAGACCCACAGATAATTTCTGCTTAAAGTCTTAACAGCACA	721
DB	699	GTTCGGTTTGGGAGCACAAGACCCACAGATAATTTCTGCTTAAAGTCTTAACAGCACA	758
QY	722	TCTGCTTGAACCACTGCTCAGATGCGCTTGGCTGAGGTGCAAGCACTGAAC---CGGA	781
DB	759	TCAGGCTTGAACCACTGCTCAGATGCGCTTGGCTGAGGTGCAAGCACTGAAC---CGGA	818
QY	782	TCCTTTTTCATCAATGTTGGTGAAGCTCTTACAGGTAATGACTTAATGGGAGGTTTAAAGT	841
DB	819	TCCTTTTTCATCAATGTTGGTGAAGCTCTTACAGGTAATGACTTAATGGGAGGTTTAAAGT	878
QY	842	GTAAAGCATAGGTTTGGCTGACACAAGCAAGTCAAGGTTATCAATGATCTACTTTTGA	901
DB	879	GTAAAGCATAGGTTTGGCTGACACAAGCAAGTCAAGGTTATCAATGATCTACTTTTGA	938
QY	902	GGACCAAGGTTGAGTGAATAATAGCAGCTTTACCTTCAGTGCATGTTAAAGGAGGAG	961
DB	939	GGACCAAGGTTGAGTGAATAATAGCAGCTTTACCTTCAGTGCATGTTAAAGGAGGAG	998
QY	962	TGTTTGTCAAAAGAGTTCACATGTTGTGAATAACAAGAGGCTGCGTACACTTCAAGGCTA	1021
DB	999	AGTTTGTCAAAAGAGTTCACATGTTGTGAATAACAAGAGGCTGCGTACACTTCAAGGCTA	1058
QY	1022	GCTGATAATAGGCTTGGCCCTTTCAGAAATCTGCTGATTAACCAACACACCCCTTC	1081
DB	1059	GCGGATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGATTAAGGAGGCAAGGTGT	1118
QY	1082	AAA-----TTCCACTCATTTTACGACGCTGTTATTTACCCCA-----TTTTCTTCTCTTT	1132
DB	1119	CAAAATTTCTACTACTCAATTTTGGCAGCGTGTGTTAGGCCAACTTTTATTTATTTT	1178
QY	1133	TCCTTTTCTGCTGCTGCTAGGTTTCAACAGCTTCACTCTACTGACATATATAGAAAT	1192
DB	1179	TTTTTGGGTGTGTATCTAGGTTTCAACAGCTTCACTCTACTGACATATATAGAAAT	1238
QY	1193	GAATAGGT-----TAAGATGTTTATCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	1241
DB	1239	GAATAGGTGCTTATGCACTTCTTTTATCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	1298
QY	1242	TACAGTGGTCTCAACTTCCCTTTCCTCAATGTCATGGAACCGCACTCTAGTTACA	1300
DB	1299	TAAATAGT-----CACTACTGCTTCTTATTTATCAATGAACCGCACTCTAGTTACA	1349

RESULT 5

ADM94213

ID ADM94213 standard; cDNA; 1352 BP.

XX AC ADM94213;

XX AC ADM94213;

DT 17-JUN-2004 (first entry)

XX Soybean Dioxxygenase cDNA #2.

DE Soybean; se; plant; plant metabolism;

KW GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate synthase;

KW Dioxxygenase; Bnt-Kaurene Synthase A; GA-20 oxidase; deaminase;

KW Gibberellin 3-beta hydroxylase; Riboflavin specific

KW Ethylene response factor; Acyl-CoA thioesterase II;

KW ABC transporter GCN20-like; P-glycoprotein I; P-glycoprotein 3;
KW P-glycoprotein ATPGP; P-glycoprotein HVMDR2; ABC transporter;
KW PMP70 ABC transporter; MRP4 ABC transporter; transgenic.
XX
OS Glycine max.
XX

XX US6677502-B1.
XX
XX 13-JAN-2004.
XX

XX 12-JUL-2000; 2000US-00614912.
XX
XX 12-JUL-1999; 99US-0143401P.
XX 12-JUL-1999; 99US-0143412P.
XX 30-JUL-1999; 99US-0146650P.
XX 15-DEC-1999; 99US-0170906P.
XX 21-DEC-1999; 99US-0172946P.
XX 21-DEC-1999; 99US-0172959P.
XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX

XX Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Farnodu OO;
XX Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Cai MI PG, Fang Y;
XX Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
XX Li CP;
XX
XX WPI; 2004-088430/09.
XX P-PSDB; ADM94214.
XX

XX New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
XX synthase nucleic acid and proteins, useful for creating transgenic plants
XX where polypeptides are present at higher or lower levels.
XX
XX Example 3; SEQ ID NO 13; 186pp; English.
XX

XX The invention relates to an isolated polynucleotide comprising a
XX nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
XX II/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as
XX ADM94266. Also included are a vector comprising the polynucleotide, a
XX recombinant DNA construct comprising the polynucleotide operably linked
XX to at least one regulatory sequence, transforming a cell with the
XX polynucleotide, a cell comprising the recombinant DNA construct,
XX producing a plant (comprising transforming a plant cell with the
XX polynucleotide and regenerating a plant from the transformed plant cell),
XX a plant comprising the recombinant DNA construct and a seed comprising
XX the recombinant DNA construct. Also disclosed as new are nucleic acid
XX (cDNA) fragments and assembled contigs encoding plant metabolism proteins
XX chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
XX synthase, Dioxxygenase, Ent-Kaurene Synthase A, GA-20 oxidase, Gibberellin
XX 3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
XX factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-
XX glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein
XX HVMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
XX The nucleic acid fragments may be used to create transgenic plants where
XX the polypeptides are present at higher or lower levels than normal or in
XX cell types or in developmental stages in which they are not normally
XX found. The polynucleotides can be used as probes for genetically and
XX physically mapping genes and as markers for traits linked to those genes.
XX The nucleic acid fragments may be used as restriction fragment length
XX polymorphism (RFLP). It can also be used to probe Southern blots
XX containing restriction endonuclease-treated genomic DNAs of a set of
XX individuals representing parent and progeny of a defined genetic cross.
XX The nucleic acid fragments may also be used as hybridisation probes
XX against PCR amplification products generated from the mutation population
XX using the mutation tag sequence primer in conjunction with an arbitrary
XX genomic site primer. The peptides can also be used to immunise animals to
XX produce polyclonal or monoclonal antibodies with specificity for peptides
XX or proteins comprising the amino acid sequences. Antibodies are useful
XX for detecting the polypeptides in situ in cells or in vitro in cell
XX extracts. The present sequence encodes a plant metabolism protein (or
XX fragment).
XX

SQ Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;
Query Match 32.7%; Score 430.8; DB 12; Length 1352;
Best Local Similarity 65.7%; Pred. No. 1.2e-108;
Matches 665; Conservative 0; Mismatches 332; Indels 15; Gaps 2;
QY 55 AACACAAACCAACCATGGTTGTCTCTCAGCCAGCATTTGAACCAAGTCTTCTCTCTGAA 114
DB 146 AACACAAAGAAAATGGTGTGTGTCTCAAGCAACACAGAACATCTCTACATTA 205
QY 115 ACCATTCAAGTCCACGCCCTTGTTCACGGGAGATTCCTGTGTGTCGACCTCAGCAGCCCGA 174
DB 206 GAACTGCATGCCAACCAAAATTTCTCTCAACAATTTCCATAGTGGACCTCTCAAACTGA 265
QY 175 TGCCAGAATCTCATAGTGAAGCCCTGTAGGACCTTCGGCTTCTCAAGCTGTGTGAACCA 234
DB 266 TGCAAGAGCCCTTATAGTGAAGCTTGTGAGGAGTTTGGATTTCTCAAGTCTCAATCA 325
QY 235 TGTGTTCCTCAATTTGGAGTTAATGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAA 294
DB 326 TGTGTCTCCATGGAGCTATATCCGAATTTGGAATATGAAGCCTTCAAAATTTCTCTCTAT 385
QY 295 ATCTAGTCCGAGAAAGACAGAGCTGGTCCCGCCGACCCCTTTCGGCTATGTGTAGCAAGAG 354
DB 386 GTCACCTCAATGAAAGGAAAAAGTAGGACCTCCCAATCCATTTGGGTATGTGTAGCAAGAA 445
QY 355 GATTGGCCCAACCGGTGATGCTGGTGGCTCGAATACCTCTCCCTCAACACCAACCCCTGA 414
DB 446 AATTGGACACAATGGGGAGCTTGGTTGGATTGAGTACCTTTCTCTCAACACCAATCAAGA 505
QY 415 TGTATTCTCACCAAAATCACTTTTGGCAATTTTCGAGAAAAATTCCTCATCTTTTCAGGGCGGT 474
DB 506 ACACAACT-----TCTCTGTTTATGGAAAAACCCCTGAGAAATTCAGGTTGCT 553
QY 475 GGTGGAGAACTACATTACAGCAGTGAAGAAATGTGCTATGCGGTGTTGGAAATTTGATGCG 534
DB 554 GTTGAACAGTTACATGTCTTCTGTGAGGAAGATGGCATGTGAGATTCTTTGAGTTGATGCG 613
QY 535 CGAGGGTTGGGGATAAGCAGAGGAATACGTTTAGCAGGTTGCTCAAGAGTGAAGAAAG 594
DB 614 AGAAGGTTGAAGATTCAGCAAAAGAGTGTGTTTAGCAAGCTTCTAATGGATTAACAAAG 673
QY 595 TGATTCGTCTCTCAGGTTGAACCACTACCCCGCTTGCCTCGAGGTGCAAGCACTGAACCG 654
DB 674 TGACTCTATTTTCAGGGTGAATCATTTACCTCTGTTCTCGAAATGACTCTGAATGATCA 733
QY 655 GAATTTGGTTGGGTTGGGAGACACAGACCCACAGATAAATTTCTGTCTTAAATCTAA 714
DB 734 GAACTTGAATGGGTTTGGAGAAACACAGACCCCAAAATCATCTCTCTGTTAAGATCCAA 793
QY 715 CAGCACATCTGGCTTGCAAATCTGTCTCACAGATGSCACTTGGGTTTCAGTCCACCTGA 774
DB 794 CAACACTTCAGGCTTCAGATTATCTTAGAATGGAATTTGATTTCAAGTCCACCAAG 853
QY 775 TCAGACTCTCTTTTTCATCAATGTTGGTGACCTCTTACAGGTAATGACTTAATGGGAGTT 834
DB 854 TGACAAATCTCTTTTATTAACTGTTGTTGTTCTCTCAGGTTATGACAAATGGAAGTT 913
QY 835 TAAAGTGTAAAGCATAGGTTTGGCTGACACACAGAAAGTCAAGTTATCAATGATCTA 894
DB 914 CCGAAGTTGTGAGACACAGAGTGTGGCAAAATGGGTTTCAAGTCCAGGCTTTCAATGATTA 973
QY 895 CTTTGGAGACCAAGCGTTTCAGTGAATAATAGCACCTTTACCTTCAGTGTGTTAAAGG 954
DB 974 CTTTGGAGTCCACCTTTGAGTGAGAAATAGCAACCATTTATCTCTCTCATG---AAAGG 1030
QY 955 AGAGGAGTGTGTTGTACAAAGAGTTTCAATGGTGTGTAATACAAAGAGGTCGCTACATCTC 1014
DB 1031 AAAGAAAGTCTATATAAAGAGTTTACCTGGTTTGGAGTACAAAAATCAATCTACGGTTC 1090
QY 1015 AAGGCTAGCTGATTAATAGGCTTGCCTCTTTCAGAAATCTGCTGCTGATTA 1066
DB 1091 AAGATTATCTAAAAATAGACTTTGAACATTTTGAAGAATTTGCAGCTTCGTAA 1142

RESULT 6

ADW94205
 ID ADM94205 standard; cDNA; 1365 BP.
 AC ADM94205;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Soybean Dioxygenase cDNA #1.
 XX
 KW Soybean; ss; plant; plant metabolism;
 KW GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase;
 KW Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase;
 KW Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;
 KW Ethylene response factor; Acyl-CoA thioesterase II;
 KW ABC transporter GN20-like; P-glycoprotein I; P-glycoprotein 3;
 KW P-glycoprotein ATPGP; P-glycoprotein HVMR2; ABC transporter;
 KW PMP70 ABC transporter; MRP4 ABC transporter; transgenic.
 XX
 OS Glycine max.
 XX
 PN US6677502-B1.
 PD 13-JAN-2004.
 XX
 PF 12-JUL-2000; 2000US-00614912.
 XX
 PR 12-JUL-1999; 99US-0143401P.
 PR 30-JUL-1999; 99US-0143412P.
 PR 30-JUL-1999; 99US-0146650P.
 PR 15-DEC-1999; 99US-0170906P.
 PR 21-DEC-1999; 99US-0172946P.
 PR 21-DEC-1999; 99US-0172959P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO B I.
 PA (PION-) PIONEER HI-BRED INT INC.
 PI Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
 PI Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Caiami PG, Fang Y;
 PI Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Heientjaris TG;
 PI Li CP;
 DR WPI; 2004-088430/09.
 DR P-PSDB; ADM94206.
 XX
 PT New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
 PT synthase nucleic acid and proteins, useful for creating transgenic plants
 PT where polypeptides are present at higher or lower levels.
 XX
 PS Example 3; SEQ ID NO 5; 186pp; English.
 CC The invention relates to an isolated polynucleotide comprising a
 CC nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
 CC II/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as
 CC ADM94266. Also included are a vector comprising the polynucleotide, a
 CC recombinant DNA construct comprising the polynucleotide operably linked
 CC to at least one regulatory sequence, transforming a cell with the
 CC polynucleotide, a cell comprising the recombinant DNA construct,
 CC producing a plant (comprising transforming a plant cell with the
 CC polynucleotide and regenerating a plant from the transformed plant cell),
 CC a plant comprising the recombinant DNA construct and a seed comprising
 CC the recombinant DNA construct. Also disclosed as new are nucleic acid
 CC (cDNA) fragments and assembled contigs encoding plant metabolic proteins
 CC chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
 CC synthase, Dioxygenase, Ent-Kaurene Synthase A, GA-20 oxidase, Gibberellin
 CC 3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
 CC factor, Acyl-CoA thioesterase II, ABC transporter GN20-like, P-
 CC glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein
 CC HVMR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
 CC The nucleic acid fragments may be used to create transgenic plants where
 CC the polypeptides are present at higher or lower levels than normal or in

cell types or in developmental stages in which they are not normally
 found. The polynucleotides can be used as probes for genetically and
 physically mapping genes and as markers for traits linked to those genes.
 The nucleic acid fragments may be used as restriction fragment length
 polymorphism (RFLP). It can also be used to probe Southern blots
 containing restriction endonuclease-treated genomic DNAs of a set of
 individuals representing parent and progeny of a defined genetic cross.
 The nucleic acid fragments may also be used as hybridisation probes
 against PCR amplification products generated from the mutation population
 using the mutation tag sequence primer in conjunction with an arbitrary
 genomic site primer. The peptides can also be used to immunise animals to
 produce polyclonal or monoclonal antibodies with specificity for peptides
 or proteins comprising the amino acid sequences. Antibodies are useful
 for detecting the polypeptides in situ in cells or in vitro in cell
 extracts. The present sequence encodes a plant metabolism protein (or
 fragment).
 XX
 SQ Sequence 1365 BP; 448 A; 258 C; 244 G; 415 T; 0 U; 0 Other;
 Query Match 32.6%; Score 429.2; DB 12; Length 1365;
 Best Local Similarity 65.6%; Pred. No. 3.3e-108;
 Matches 664; Conservative 0; Mismatches 333; Indels 15; Gaps 2;
 QY 55 AACACACACACACACATGGTGTCTCTCAGCCAGCATTGACCAAGTTTCTCTCTGAA 114
 DB 153 AACACACACACACACATGGTGTCTCTCAGCCAGCATTGACCAAGTTTCTCTCTGAA 212
 QY 115 ACCATTCAAGTCCACGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCACGCCACCCCA 174
 DB 213 GAATGCGATGCCAACCAATTTTCTCAACAATCCATAGTGGACCTCTCCAAACCTGA 272
 QY 175 TGCCAAGAATCTCAGTAGTGAAGCCGTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACCA 234
 DB 273 TGAAGAAGACCTTATAGTGAAGGCTTGTGAGAGTTTGGATTCTTCAAAAGTCATCAATCA 332
 QY 235 TGGTGTTCATTTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAA 294
 DB 333 TGGTGTCTCCATGGAGCTATATCCGAATTTGAATATGAAGCCTTCAAAATTTCTTCTAT 392
 QY 295 ATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCGCCACCTTTCGGCTATGTGTAGCAAGAG 354
 DB 393 GTCACTCAATGAAGAAGAAAGTAGGACCTCCCAATCCATTTGGGTATGTGTAGCAAGAA 452
 QY 355 GATTGGCCCCAAACGGTGATGTGGTGGGTGAATACCTCTCTCAACACCAACCCCTGA 414
 DB 453 AATTGGACACAATAGGGACGTTGGTGGATTGAGTACCTTCTTCAACACCAATCAAGA 512
 QY 415 TGTATCTCACCAATCACTTTGCAATTTTCGAGAAATTCCTCATCTTTCAGGGCGGT 474
 DB 513 ACACAAC-T-----TCTCTGTTTATGGCAAAAACCCCTGAGAAATTCAGGTGTCT 560
 QY 475 GGTGAGAACTACATTACAGCAGTGAAGAAACATGTGCTATGGGTTTGGAAATTTGATGGC 534
 DB 561 GTTGAACAGTTACATGCTCTTCTGAGGAAGATGCGATGTGAGATCTTGAGTTGATGGC 620
 QY 535 GGAGGGTTGGGGATAAGCAGAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAG 594
 DB 621 AGAAGGGTTGAAGATTACGACAAAAGGATGTGTTTGAAGAGCTTCTAATGGATAAACAAAG 680
 QY 595 TGATTCTGCTTTCAGGTTGAACCACTACCGGCTTGGCCCTGAGGTGCAAGCACTGNAACCG 654
 DB 681 TGACTCTATTTTTCAGGGTGAATCATTTACCTGCTGCTGAAATGACTCTGAAATGATCA 740
 QY 655 GAATTTGGTGGTGGTGGGAGCACACAGACCCACAGATAAATTTCTGCTTAAAGATCTAA 714
 DB 741 GAACTTGATGGGTTGGAGAAACACAGACCCCAAAATCATCTCTCTGTTAGATCCAA 800
 QY 715 CAGCACATCTGGCTTGCAAAATCTGTCTCACAGATGGCACTTGGGTTTCACTCCACCTGA 774
 DB 801 CAACACTTCAGGCTTCAGATTTTATCTTAGAGATGGAATTTGATTTTCACTCCACCA 860
 QY 775 TCAGACTTCTCTTTTTCATCAATGTTGGTGACCTCTACAGGTAATGACTAATGGGAGGTT 834

Db 861 TGACAAATCCTTTTATTAACGTTGGTGATCTCTTCAGGTATGACAAATGGAAGTT 920
 QY 835 TAAAGCTGTAAAGCATAGGTTTGGCTGACACAAAGAGTCAAGGTATCAATGATCTA 894
 Db 921 CCGAAGTGTAGACACAGAGTGTGGCAATGGGTTCAAGTCCAGGCTTTCATGATTTA 980
 QY 895 CTTTGAGGACCAAGCCTTGAGTGAATAATAGCACCTTTTACCTTCAGTGTATTAAGG 954
 Db 981 CTTTGAGGTCACCTTTCAGTGAGAAATAGCACCATTTCTCTCATG---AAAGG 1037
 QY 955 AGAGGAGTCTTTGTACAAAGAGTTCATGCTGATGATCAAGAGGCTGCGTACACTTC 1014
 Db 1038 AAAAGAAAGTCTATATAAAGAGTTTACCTGGTTTGAGTACAAATAATCAATCTACGGTTC 1097
 QY 1015 AAGGCTAGCTGATAATAGGCTTGCCCTTTCCAGAAATCTGCTGCTGATTAA 1066
 Db 1098 AAGATTATCTAATAATAGACTTGAACATTTTGAAGAATTCAGCTTCGTAA 1149

RESULT 7
 ID AAZ55916 standard; cDNA; 1237 BP.
 XX AAZ55916;
 XX 10-APR-2000 (first entry)
 DT Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA.
 DE Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA.
 KW Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
 KW growth inhibition; ss.
 XX Arabidopsis thaliana.

Key Location/Qualifiers
 CDS 109..1134
 FT /*tag= a
 FT /product= "Gibberellin 2-oxidase AtGA2ox2"
 XX WO9966029-A2.
 XX 23-DEC-1999.
 XX 11-JUN-1999; 99WO-GB001857.
 XX 12-JUN-1998; 98GB-00012821.
 XX 15-JUL-1998; 98GB-00015404.
 XX (UYBR-) UNIV BRISTOL.
 XX Thomas SG, Hedden P, Phillips AL;
 XX WPI; 2000-097742/08.
 DR P-PSDB; AAY58599.
 XX New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
 PT to produce transgenic plants with improved or altered growth
 PT characteristics.
 XX Example 3; Fig 7; 42pp; English.

This sequence represents cDNA encoding an Arabidopsis thaliana
 gibberellin (GA) 2-oxidase, PcGA2ox2. This enzyme is a GA 2-beta-
 hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is
 its only activity. Hydroxylation at the 2-beta position of a GA results
 in a biologically inactive product, and is the most important route for
 GA metabolism in plants, ensuring that the active hormones do not
 accumulate in plant tissues. The nucleic acids can be used to transform
 plants so that gibberellin 2-oxidase can be constitutively over-expressed
 or otherwise enhanced to reduce the concentration of bioactive GAs in the
 plants and therefore to inhibit plant growth. Growth inhibition is useful
 in many agricultural and horticultural applications such as enhancing
 lodging-resistance and grain yield in cereals, improving seedling

CC quality, reducing the growth of amenity grasses, reducing shoot growth in
 CC orchard and ornamental trees, improving tolerance to cold, drought and
 CC infection, and increasing yields (by the diversion of assimilates from
 CC vegetative to reproductive organs). The nucleic acids may also be used to
 CC induce male and/or female sterility (by expression in floral organs),
 CC prevent pre-harvest sprouting, reduce shoot growth in hedging plants,
 CC inhibit reversibility in the development or germination of seeds and
 CC reduce shoot growth in commercial wood species. Antisense constructs of
 CC the nucleic acids can also be used to transform plants to reduce the
 CC expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
 CC improve fruit set and growth in seedless grapes, citrus fruits and
 CC pears), improve skin texture and fruit shape in apples, increase stem
 CC length and therefore yield in sugar cane, increase yield and earliness in
 CC celery and rhubarb, improve malting yields and quality in cereals
 CC (particularly barley), and increase growth in woody species
 XX
 SQ Sequence 1237 BP; 356 A; 277 C; 280 G; 324 T; 0 U; 0 Other;

Query Match 32.3%; Score 425.8; DB 3; Length 1237;
 Best Local Similarity 66.3%; Pred. No. 2.8e-107;
 Matches 629; Conservative 0; Mismatches 317; Indels 3; Gaps 1;
 QY 146 ATTCTGTGTCGACCTCAGGCACCCCGATGCCAAGAATCTCATAGTGAACGCTTAGG 205
 Db 199 ATCCCGCTGTCACACCTAGCCGATCCGGAAGCGAAACCCGAAATCGTAAAGCCTCGGAG 258
 QY 206 GACTTCGGCTTCTCAAGCTTGTGAACCATGTGTTCCTTCCATTTGAGTAAATGGCAATTTA 265
 Db 259 GAGTTCCGGTCTTCAAGTCTGTAACACCGAGTCCGACCGAATCTCATGACTCGGTTA 318
 QY 266 GAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAAGACAGAGCTGTGCC 325
 Db 319 GAGCAGGAGGCTATTGGCTTCTTCGGCTGCTCAGTCTCTTAAAAACCGGCGGTCCA 378
 QY 326 CCGGACCTTTCGGCTATGTTAGCAAGAGGATTTGCCCAACCGTGTATGTCGGTTGGGTC 385
 Db 379 CCTGAACCGTACGTTATGTTAATAACCGATTGGACCAACCGGTGACGCTTGGTTGGATT 438
 QY 386 GAATACCTCTCTCAACACCAACCTGATGTTATCTCACCCCAATCACTTTGTCATTTTC 445
 Db 439 GAGTATCTCTCTCAATGCTAATCTCTCAGTCTCTCTCTTAAACCTCCCGCGCTTTC 498
 QY 446 CGAGAAATCTCTCATCATTTTCAGGGCGGTGGTGGAGAACTACATTCACGACGTGAAGAAC 505
 Db 499 CGTCAAAACCCCTCAAAATTTTCGTCGAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 558
 QY 506 ATGTGCTATGCGTGTGGAATTTGATGGCGGAGGGTTGGGATAGGACAGGAGATACG 565
 Db 559 GTGTCGTACAGGTTGTTGGAGATGGTTGCCGAAGAACTAGGATAGAGCCAAAGGACACT 618
 QY 566 TTAAGCAGGTTGCTGAAGGATGAGAAAAGTATTCGTGCTTCAGGTTTGAACCACTACCCG 625
 Db 619 CTGAGTAAATGCTGAGAGATGAGAAAGATGACTGTCGCTGAGACTAAACCAATATTCG 678
 QY 626 CTTTGCCCTTGAGTGCACACTGAAACCGGAATTTTGGTTGGGTTTGGGAGGACACACAGAC 685
 Db 679 GCG---GCGGAGGAGAGCGCGGAGAGATGGTCAGGTGGGGTTTGGGGAACACACAGAC 735
 QY 686 CCACAGATAATTTCTGCTTTAAGATCTAACAGCACATCTGGCTTGCAGAAATCTGCTCTACA 745
 Db 736 CCACAGATAATCTCAGTGTCTAAGATCTAATAACACGCGCGGCTCTTCAAAATCTGTGTGAA 795
 QY 746 GATGGCACTTGGTGTTCAGTCCCACTGATCAGACTTCTCTTTTCAATCAATGTTGTGAC 805
 Db 796 GATGGAAGTTGGTTCGCTGCTCTCTGATCACTCTTCTTCTTCAATTAATGTTGAGAT 855
 QY 806 GCTCTACAGGTAATGACTAATCGGAGTTTAAAGTGTAAAGCATAGGTTTGGGTGAC 865
 Db 856 GCTCTTCAGGTTGACTAAACGAGGTTTCAAGAGTGTAAACACACAGGCTCTTAGCCGAT 915
 QY 866 ACAACGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCGCTTGTGATGAATAATA 925
 Db 916 ACAAGGAGATCGAGGATTTCAATGATATATTTTCGGCGGACCGCCATTGAGCCAGAGATC 975

Qy	926	GCACCTTTACCTTCAGTGATGTTAAAGGAGAGAGAGTGTTCATCAAGAAGTTCACATGG	985
Db	976	GCACCAATTGGCATGCGCTTGTCCTTGACGACAGATGATTGGCTTTACAAGAAGTTCACCTGG	1035
Qy	986	TGTGAATACACAAGAGGCTGGCGTACACTTCAAGGCTAGCTGATTAATAGCTTGCCCTTTC	1045
Db	1036	TCTCAATACAAATCTTCTGCTTCAAGCTCTAAGCTGGTGATATAGACTTGGTCTCTTT	1095
Qy	1046	CAGAAATCTGCTGCTGATTAACCAACACACCCCTTCAAATCCACTCAT	1094
Db	1096	GAGAAACAACCTCTTCTCAATCATAAACCCCTTGATGAGAGTAGTCAT	1144

RESULT 8

ABZ13545
ID ABZ13545 standard; DNA; 1026 BP.

Qy	206	GACTTCGGCTCTTCAAGCTTGTGAACCAATGGTGTCCATTGGAGTTAAATGGCCAAATTTA	265
Db	151	GAGTTCCGGGTCTTCAAGGTTCGTAACACCGGAGTCGACCCGAACTCATGACTTCGGTTA	210
Qy	266	GA AAAAGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGTGCC	325
Db	211	GAGCAGGAGCTATTGGCTTCTTCGGCTTGCCTCAGTCTCTTAAAAACCGGCCCGTCCA	270
Qy	326	CCGACCCCTTTCGGCTATGTGTAGCAAGAGATTTGGCCCAAAACGGTGATGTTCGGTTGGGTC	385
Db	271	CCTGAACCGTACCGTTATGTGTATTAACGGAITTTGGACCAACCGTGACGTTGGTTGGATT	330
Qy	386	GAATACCTCTCCTCAACACCAACCCCTGATGTTATCTCACCCAAATCACTTTGCATTTTC	445
Db	331	GAGTATCTCTCTCAATGCTAATCTCAGCTCTCTCTCTCTAAAACCTCGCGCGTTTC	390
Qy	446	CGAGAAATCCTCATCATTTTCAGGGCGGTGGTGAGAACTACATTAACAGCAGTGAAGAAC	505
Db	391	CGTCAAAACCCCTCAAAATTTTCCGTGAGTCGGTGGAGGAGTACATGAAGGAGATTTAAGGAA	450
Qy	506	ATGTGCTATCGGTTGTGGAAATTTGATGGCGGAGGGTTGGGGATTAAGCGAGAGGAATACG	565
Db	451	GTGTGCTACAAGGTGTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCCAAAGGCACT	510
Qy	566	TTAAGCAGGTTGCTGAAGGATGAGAAAGTGAATTCGTGCTTCAGGTTTGAACCACTACCCG	625
Db	511	CTGAGTAAATGCTGAGAGATGAGAAGTGAATCTCGTGCTCGAGACTAAACCAATATCCG	570
Qy	626	CCTTGGCCCTGAGTGCNAGCACTGAACCGGAAATTTGGTTGGGTTTGGGAGCACACAGAC	685
Db	571	GC---GCGCGAGAAAGAGCGGAGAGATGGTGAAGGTGGGGTTGGGGAAACACACAGAC	627
Qy	686	CCACAGATAATTTCTGTCTTTAAGATCTAACAGACACATCTGGCTTGCAAATCTGTCTCACA	745
Db	628	CCACAGATAATCTCAGTGCTAAGATCTAATAACACGGCGGGTCTTCAATCTGTGTGAA	687
Qy	746	GATGGCACTTGGGTTTCAGTCCCACTGTATCAGACTTCCTCTTTTTCATCAATGTTGGTGAC	805
Db	688	GATGGGAAGTTGGGTGCGTGTCCCTCTGTATCACTCTTCTTTCTTCAATTAATGTTGGAGAT	747
Qy	806	GCTCTACAGGTAATGACTAATGAGGAGTTTAAAGTGTAAAGCATAGGGTTTTGGGCTGAC	865
Db	748	GCTCTTCAGGTTATGACTAAACGGAGGTTCAAGAGTGTAAACACAGGGTCTTAGCCGAT	807
Qy	866	ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACAGCGTTTGAAGTGAATAATATA	925
Db	808	ACAAGGAGATCGAGGATTTCAAATGATATAATTCGGCGGACCGCCATTTGACCGAGAATC	867
Qy	926	GCACCTTTACCTTCAGTGATGTTTAAAGGAGAGGAGTGTGTGTACAAAGAGTTCACATGG	985
Db	868	GCACCAATGCGCATGCGCTTGTCCCTGAGCAAGATGATTTGGCTTTTACAAGAAATTCACATTG	927
Qy	986	TGTGAATACAAAGAGGCTCGGTACACTTCAAGGCTAGCTGATTAATAGGCTTTCGCCCTTTC	1045
Db	928	TCTCAATACAAATCTCTCTGCTTACAGTCTAAGCTTGGTGTATATAGACTTGGTCTCTTT	987
Qy	1046	CAGAAATCTGCTGTGATTAACCAACACAC	1076
Db	988	GAGAAACAACTCTTCTCAATCATAAACCC	1018

RESIST 9

RESOL 9
ADA67975
ID ADA67975 standard; DNA; 1026 BP.

CC expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
CC improve fruit set and growth in seedless grapes, citrus fruits and
CC pears), improve skin texture and fruit shape in apples, increase stem
CC length and therefore yield in sugar cane, increase yield and earliness in
CC celery and rhubarb, improve malting yields and quality in cereals
CC (particularly barley), and increase growth in woody species
XX

SQ Sequence 1008 BP; 296 A; 212 C; 232 G; 268 T; 0 U; 0 Other;

Query Match 29.0%; Score 382.8; DB 3; Length 1008;
Best Local Similarity 64.1%; Pred. No. 2.2e-95;
Matches 595; Conservative 0; Mismatches 327; Indels 6; Gaps 1;

QY	146	ATTCTGTGGTTCGACCTCAGCACCCGATGCCAAGAATTCATAGTGAACCCCTGTAGG	205
DB	79	ATCCCTGTTATAGACTTAAACCGACTCAGATGCCAAACCCAAATCGTCAAGCATGTGAA	138
QY	206	GACTTCGGCTTCTTCAGCTTGTGAACCATGTTCCATTGGAGTTAATGCCAATTTA	265
DB	139	GAGTTTGGGTTCTTCAAGTGTCAACCATGGGTCGACCCCGATCTTTTGACTCAGTTG	198
QY	266	GAACACGAGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGAACACAGAGCTGTGCC	325
DB	199	GAGCAGAAGCCATCACTCTTTTGGTCATCTCTCAAGACAAAGCGGTCCA	258
QY	326	CCCGACCCCTTCGGCTATGTTAGCAAGAGGATGGCCCAACCGTGATGCGTTGGGTC	385
DB	259	CCTGACCCGTTTGGTTACGGTACTAAAGGATGGACCCCAATGGTGACCTTGGCTT	318
QY	386	GAATACCTCTCTCAACCAACCCCTGATTTATCTCAACCAATCATCTTTGCAATTTTC	445
DB	319	GAGTACATTTCTCTTAATGCTAATCTTTTGGCTTGAAGTCTCACAAAACCCGCCATTTTC	378
QY	446	CGAGAAATCCCTCATCTTTCAGGGGGGTTGGAGAACTACATTACAGCAGTGAAGAAC	505
DB	379	CGCACACCCCTGCAATTTTCAGAGGCGAGTGGAGAGTACATTAAAGATTAAGAGA	438
QY	506	ATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGTTGGGATAGGCGAGGGAATAGC	565
DB	439	ATGTGCGCAAAATTTCTGGAATTTGTAGAGGAAGAGCTAAAGATAGAGCCAAAGAGAAG	498
QY	566	TTAAGCAGGTGCTGAGGATGAGAAAGTATGTTGCTTCAGTTGAAACACATACCGG	625
DB	499	CTGAGCCGTTTGGTGAAGATGAAGAAAGTATGTTGCTGAGATGAACCATTTACCGG	558
QY	626	CCTTGCCTGAGTGCACACCTGAAACCGAATTTGGTTGGTTGGGGAGCACACAGAC	685
DB	559	-----GAGAAGAGAGAGACTCGGTCAAGGAAGAGATTGGGTTCGGTGACACACTGAT	612
QY	686	CCACAGATAATTTCTGCTTTAAGATCTAACAGCAGCATCTGGCTTGCAAACTGTCTCA	745
DB	613	CCACAGTTGATATCACTGCTCAGTCAAAAGCAGACAGAGGGTTTGCAAATCTGTGTC	672
QY	746	GATGGCATTGGGTTTCAGTCCCACTGATCAGACTTCTTTTCAATCAATGTTGGTGAC	805
DB	673	GATGGAACATGGGTTGATGTTACCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT	732
QY	806	GTCTACAGTAACTAATGGAGGTTTAAAGTGAAGCATAGGTTTGGCTGAC	865
DB	733	ACTTTTCAGTGATGACAAACGGAAGATTCAGAGTGTGAACATAGAGTGGTGACAAAT	792
QY	866	ACAAAGAGTCAAGGTTTATCAATGATCTACTTTTGGAGGACCGGTTGAGTGAAATATA	925
DB	793	ACAAAGAGTCAAGGATATCGATGATCTACTTCGACAGTCTCTCTTGGAGCGAAGATT	852
QY	926	GCACCTTACCTTCAGTATGTTAAAGAGAGGAGTGTGTTGACAAAGATTCACATGG	985
DB	853	GCACCATTTATCATGCTTGTGCAAGCAAGATGATTGCTTTTATAATGAGTTTACTGG	912
QY	986	TCTGATACAGAGGCTCGGTACCTTCAAGGCTAGCTGATAATAGGCTTCCCTTTTC	1045
DB	913	TCTCAATACAGATTATCTGCTTACAAAATAAGCTTGGTGACTATAGGCTTGGTCTCTTT	972

QY 1046 CAGAAATCTGCTGCTGATTAAACCAACA 1073
DB 973 CAGAAACGACCTCCATTTTCTATCCA 1000

RESULT 13

ADM94207
ID ADM94207 standard; cDNA; 1473 BP.

XX AC ADM94207;

XX DT 17-JUN-2004 (first entry)

XX DE Wheat Dioxygenase cDNA #1.

XX KW Wheat; ss; plant; plant metabolism;

KW GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate synthase;

KW Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase;

KW Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;

KW Ethylene response factor; Acyl-CoA thioesterase II;

KW ABC transporter GCN20-like; P-glycoprotein I; P-glycoprotein 3;

KW P-glycoprotein ATPGP; P-glycoprotein HVMDR2; ABC transporter;

KW PMP70 ABC transporter; MRP4 ABC transporter; transgenic.

XX Triticum aestivum.

XX US6677502-B1.

XX PD 13-JAN-2004.

XX PF 12-JUL-2000; 2000US-00614912.

XX PR 12-JUL-1999; 99US-0143401P.

XX PR 12-JUL-1999; 99US-0143412P.

XX PR 30-JUL-1999; 99US-014650P.

XX PR 15-DEC-1999; 99US-0170908P.

XX PR 21-DEC-1999; 99US-0172946P.

XX PR 21-DEC-1999; 99US-0172959P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.
(PION-) PIONEER HI-BRED INT INC.

PI Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Fanodu OO;

PI Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;

PI Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;

PI Li CP;

XX WPI; 2004-088430/09.

DR P-PSDB; ADM94208.

XX New isolated GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate
synthase nucleic acid and proteins, useful for creating transgenic plants
where polypeptides are present at higher or lower levels.

XX Example 3; SEQ ID NO 7; 186pp; English.

XX The invention relates to an isolated polynucleotide comprising a
nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
II/3, 4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as
ADM94286. Also included are a vector comprising the polynucleotide, a
recombinant DNA construct comprising the polynucleotide operably linked
to at least one regulatory sequence, transforming a cell with the
polynucleotide, a cell comprising the recombinant DNA construct,
producing a plant (comprising transforming a plant cell with the
polynucleotide and regenerating a plant from the transformed plant cell),
a plant comprising the recombinant DNA construct and a seed comprising
the recombinant DNA construct. Also disclosed as new are nucleic acid
(cDNA) fragments and assembled contigs encoding plant metabolism proteins
chosen from GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate
synthase, Dioxygenase, Ent-Kaurene Synthase A, GA-20 oxidase, Gibberellin
3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-
glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein

PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
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PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161408P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.

Query Match		27.1%;	Score 356.6;	DB 3;	Length 1316;
Best Local Similarity		63.2%;	Pred. No. 4.6e-88;		
Matches 586;		Conservative 0;	Mismatches 329;	Indels 12;	Gaps 2;
QY	132	CCTGTGTTACGGGGATTCCGTGGTGCACCTCAGCACCCCGCATGCCAAGATCTCATAG	191		
DB	78	CGGGTTCCTCTAATCCCGTTATAGATATGTGACCCAGAATCCAAACATGCCCTCG	137		
QY	192	TGAAGCCCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTTCTCCATTGGAGT	251		
DB	138	TGAAGCATGCCAAGACTTCGGCTTCTTCAAGTGATCAACCATGGGTTCCGCAGAGC	197		
QY	252	TAATGCCAATTTAGAAAAGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAG	311		
DB	198	TAGTCTCTGTTTTAGAACACGAGACCGGTGATTTCTTCTCGTTGCCAAGTCAGAGAAA	257		
QY	312	ACAGAGCTGGTCCCGGACCTTTTCGGCTATGTAGCAAGAGGATTCGCCCAACGGTG	371		
DB	258	CCAAAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAAGATGGTCGGAATGGTG	314		
QY	372	ATGCGGTTGGGTGCAATACCTCTCCTCAACACCAACCCCTGATGTATCTCACCCAAAT	431		
DB	315	ACGTGGTTGGGTGAGTACTTGTGATGAACGCTAATCATGATTCGGGTCGGGTCAC	374		
QY	432	CACTTTGCATTTTCCGAGAAATCTCATCATTTAGGGCGGTGGTGAGAACTACATTA	491		
DB	375	TATTTCCAAGTCTTCTCAAAAGCCGGGAACTTTTCAGAAACGCAATTGGAAGAGTACAA	434		
QY	492	CAGCAGTGAAGACATGTCTATCGGTGTTGGATTTGATGCGGAGGGGTTGGGGATAA	551		
DB	435	CATCAGTGAGAAAAATGACATTCGATGTTTTGGAGAAAGTACACATGGGCTAGGGTCA	494		
QY	552	GGCAGAGGAATACGTTAAGCAGGTTGCTGAAGAGTGAGAAAAAGTATTGCTTCAGGT	611		
DB	495	AACCGAGGACACACTTAGCAGCTTGTGTCTGACCAAAACACGACTCGATATTGAGAC	554		
QY	612	TGAACCACTACCCGCTTGCCCTGAGGTGCAAGCACTGAAC-----CGGAATTTGG	662		
DB	555	TAAATCACTATCCACCATGCTCTTAGCAATAAGAAAAACCAATGGTGAAGATGTGA	614		
QY	663	TTGGGTTTGGGAGACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACACACAT	722		
DB	615	TTGGTTTTGGTGAACACACAGATCTCCTCAATCATCTGTCTTAAGATCTAACACACTT	674		
QY	723	CTGGCTTGCAATCTGTCTCACAGATGGCACTTGGGTTTTCAGTCCACCTGATCAGACTT	782		
DB	675	CTGGTCTCCAAATTAATCTAAATGATGGCTCATGGATCTGTCTCCTCCGATCACATT	734		
QY	783	CCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGAGGTTTAAAAAGTG	842		
DB	735	CCTTCTTCTTCAACGTTGGTGACTCTCTCCAGGTGATGACAAATGGGAGTTTCAAGAGCG	794		
QY	843	TAAAGCATAGGTTTGGCTGACACACAGAACTCAAGTTATCAATGATCTACTTTGGAG	902		
DB	795	TCAGGCATAGGTTTTTATGCTAACTGTGTAATACTAGGGTTTCTATGATTTACTTTCGCTG	854		
QY	903	GACCAAGCTTGTAGTGAATAATAGCACCTTTTACCTTCAGTGATGTTAAAGAGGAGGAGT	962		
DB	855	GACCTTCATTGACTCAGAAATCGCTCCGTTGACATGTTTGTATGACATGAGGACGAGA	914		
QY	963	GTTTGTACAAAGATTACATGGTGTGAATACAAAGGCTCGGTACACTTCAAGGCTAG	1022		
DB	915	GGTTGTACGAGGATTACTTGGTCTGAATACAAAACTCTACCTACAACTCTAGATTGT	974		
QY	1023	CTGATAATAGGTTGCCCTTTTCCAGA	1049		
DB	975	CTGATAATAGGCTTCAACAAATTCGAAA	1001		

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OM nucleic - nucleic search, using sw model

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Sequence: 1 gttctctcttaccctgt.....caaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	457	34.7	653	AW184969	se84f09.y
2	444.8	33.7	566	BM085298	sa34h07.
3	430	32.6	622	BU549366	GM880016A
4	427.4	32.4	1365	AX814544	Arabidops
5	425.8	32.3	1362	CNSOABST	Arabidops
6	422.6	32.1	1141	CNSO9V5Q	Arabidops
7	417.8	31.7	1363	CNSOABKL	Arabidops
8	386.4	29.3	1339	CNSOAC3R	Arabidops
9	378.6	28.7	612	BE802903	Arabidops
10	355.8	27.0	785	AJ803092	Arabidops
11	348.6	26.4	1128	CNSOADMV	Arabidops
12	336.2	25.5	567	BM893076	sam51f05
13	335.4	25.4	694	B1208568	ESTS26608
14	332.8	25.3	478	AL382874	Arabidops
15	329.2	25.0	893	DN589159	Arabidops
16	323.4	24.5	792	B1935635	Arabidops
17	315.8	24.0	1554	AY104425	Zea mays
18	307.8	23.4	625	CV292693	EST81070
19	307.8	23.4	642	CV292668	EST81045
20	305.8	23.2	438	BP940509	Arabidops
21	305.8	23.2	743	BG646259	EST507878
22	305.6	23.2	755	BM690134	BM690134

23	305.6	23.2	776	5	BM692820	BM692820
24	305.6	23.2	779	3	BJ571134	BJ571134
25	305.6	23.2	808	3	BJ575888	BJ575888
26	305	23.1	529	2	BG881784	ae888f09.
27	304.2	23.1	663	7	CV292717	EST81094
28	301.8	22.9	753	3	BI968577	GM830005B
29	298.6	22.7	619	1	AW584268	N210259e
30	298.2	22.6	789	5	BM685035	BM685035
31	297.6	22.6	579	6	CA844444	EA27D12a
32	297.6	22.6	724	6	CA844443	EA23G12a
33	294.6	22.4	517	3	BP074757	BP074757
34	294.6	22.4	520	3	BP074168	BP074168
35	288.6	21.9	847	8	DN982067	SV6_43H10
36	286.6	21.7	789	7	CV470333	43176.1 C
37	280.2	21.3	501	3	BP060951	BP060951
38	279.8	21.2	611	1	AW309039	ef94b04.Y
39	278.8	21.2	854	8	DN980660	SV6_28C05
40	278.4	21.1	604	7	CV630114	MdSt6013a
41	277.6	21.1	853	7	CV469374	41999.1 C
42	274.4	20.8	738	8	DN501878	V035D04.5
43	273.6	20.8	655	5	BQ404995	GA_Ed007
44	273.6	20.8	800	3	BI970132	GM830009B
45	273	20.7	685	2	BG523146	29-41 Ste

ALIGNMENTS

RESULT 1
AW184969
LOCUS
DEFINITION
se84f09.y1 Gm-c1023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1023-1410 5' similar to TR:O04162 O04162 DIOXYGENASE. ;, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Other ESTs: BU544870 corresponding to Gm-r1088-979 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1472 Std Error: 0.00
High quality sequence stop: 436.
Location/Qualifiers
1. .653
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="T157"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1023-1410"

/tissue type="seed coats of greenhouse grown plants"
/lab host="DH10B"
/clone lib="Gm-cl023"
/notes="vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
cDNA library was constructed from mRNA isolated from seed
coats (100-200mg) of greenhouse grown plants. The
library was prepared using the Life Technologies
pSuperScript cDNA library construction kit. Complementary
DNA was synthesized from mRNA using a poly (dT) sequence
with a Not I restriction site. Sal I linkers adapters
were ligated to the blunt-ended cDNA fragments followed by
Not I digestion. The cDNA fragments were directionally
cloned into the Not I-Sal I restriction site of the
pSPORT1 vector. The ligated cDNA fragments were
transformed into E.coli Electromax DH10B host cells. This
library was constructed by Dr. Lila Vodkin and Dr. Anu
Khanna."

ORIGIN

Query Match 34.7%; Score 457; DB 1; Length 653;
Best Local Similarity 87.2%; Pred. No. 2.7e-111;
Matches 499; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 65 ACCATGGTTGTTCTGCTCAGCAGCATTTGAACAGTCTTTCTCTGAAACCATTCAG 124
DB 81 ACCATGGTTGTTCTGCTCAGCAGCATTTGAACAGTCTTTCTCTGAAACCATTCAG 140

QY 125 TCCACGCCCTTGTTCAGGGGATTCCTGTGTGACCTCAGCACCCCGATGCCAAGAT 184
DB 141 CCCACGCCCTTGTTCAGGGGATTCCTGTGTGACCTCAGCACCCCGATGCCAAGAC 200

QY 185 CTCATAGTGAACGCTGTAGGACTTCGGCTCTTCAAGCTGTGAACCATGTGTCCA 244
DB 201 CACATAGTCAATGCTTCGAGGACTTCGGCTCTTCAAGCTGTGAACCATGTGTCCG 260

QY 245 TTGGAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304
DB 261 TTACAGTTTCATGGCCCAATTTGAAAAACGAAACCTCGGGTTCTTCAAAAAACCTCAATCC 320

QY 305 GAGAAAGACAGACTGGTCCCGGACCTTCGGCTATGTAGCAAGAGGATTCGCCCA 364
DB 321 GAGAAAGACAGGGCTGGTCCCGGACCTTCGGCTATGTAGCAAGAGGATTCGCCCT 380

QY 365 AACGGTGATGCGGTTGGTTCGAATACCTCCTCTCAACACCAACCTCATGTATCTCA 424
DB 381 AACGGCGATGCGGTTGGTTCGAATACCTCCTCTCAACACCAACCTCATGTATCTCC 440

QY 425 CCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTTCAGGCGGTTGGAGAAC 484
DB 441 CCCAAGTCACTGTTTTCAGAAAGGTCCTCAGAAATTCANGGCGGTTGGAGGAA 500

QY 485 TACATTACAGCAGTGAAGACATGCTATGCGGTGTGGATTTGATGGCGGGGTTG 544
DB 501 TACATTAGAGCGGTGAAGAACATGCTATGAGGTGTGGAAATGATGGTGAAGGATTTG 560

QY 545 GGATTAAGGCAGAGGAATACGTTAAGCAGGTTCTCTGAAGGATGAGAAAAGTTCGTGC 604
DB 561 TGGATAACGATAGGAATGTTGATGATGTTGCTGACGATGAGAAAGATGATTTCTTGC 620

QY 605 TTCAGGTTGAACCACTACCGCGCTTGCCTTGA 636
DB 621 TTCAGACNTTACCCTACCGCGCATTTGCCGA 652

RESULT 2
BM085298
LOCUS
DEFINITION
saj34h07.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ; mRNA
sequence.
ACCESSION
BM085298
VERSION
BM085298.1 GI:16995926
KEYWORDS
EST.

SOURCE
ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 566)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvett, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Stepcie, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.

TITLE
JOURNAL

Public Soybean EST Project

COMMENT

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 426.

FEATURES
source

1..566
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl066-4957"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week
old seedling"
/lab host="DH10B"
/clone_lib="Gm-cl066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedling from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

ORIGIN

Query Match 33.7%; Score 444.8; DB 3; Length 566;
Best Local Similarity 87.9%; Pred. No. 5e-108;
Matches 485; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 65 ACCATGGTTGTTCTGCTCAGCAGCATTTGAACAGTCTTTCTCTGAAACCATTCAG 124
DB 15 ACAATGGTTGTTTGTCTCAGCAGCATTTAAACAGTCTTTCTCTGAAACCATTCAG 74

QY 125 TCCACGCCCTTGTTCAGGGGATTCCTGTGTGACCTCAGCACCCCGATGCCAAGAT 184
DB 75 CCCACGCCCTTGTTCAGGGGATTCCTGTGTGACCTCAGCACCCCGATGCCAAGAC 134

QY 185 CTCATAGTGAACGCTGTAGGACTTCGGCTCTTCAAGCTGTGAACCATGTGTTCGA 244
DB 135 CACATAGTGAAGCCCTGCGAGGACTTCGGCTCTTCAAGCTGTGAACCATGTGTTCGA 194

QY 245 TTGGAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304

Db 195 TTAGATTTCATGGCCAAATTTGGAAACGAAACCCCTCAGGTTCTTCAAAAACCTCAGTCC 254
 QY 305 GAGAAAGACAGAGCTGGTCCCGCCAGCCCTTCGGCTATGGTAGCAAGAGGATTCGCCCA 364
 Db 255 GACAAAGACAGAGCTGGTCCCGCCAGCCCTTCGGCTATGGTAGCAAGAGGATTCGCCCT 314
 QY 365 AACGGTATGTCGGTGGTGGTGAATACCTTCCTCCTCAACACCAACCCCTGACGTATCTCA 424
 Db 315 AACGGCGATGTCGGTGGTGGTGAATACCTTCCTCCTCAACACCAACCCCTGACGTATCTCC 374
 QY 425 CCCAAATCATTGTCATTTCCGAGAAATCCTCATCTTTCAGGCGCGTGTGGAGAAC 484
 Db 375 CCCAAGTCACTGTTTCATTTCCGAGAAAGTCTCAGAAATTCAGGTGTCTTGAGGAG 434
 QY 485 TACATTACAGCAGTGAAGAACATGCTATGCTATGCGGTGTTGGAAATGATCGGAGGGTTG 544
 Db 435 TACATTAGAGCGCTGAAGAACATGCTATGCTATGCGGTGTTGGAAATGATCGGAGGGTTG 494
 QY 545 GGGATAAGCAGACGAATAGCTTAAGCAGGTGCTGAGGATGAGAAAGTGAATTCGTGC 604
 Db 495 GGAATAACTCAGAGGAATCGTTGAGTAGGTGCTGGAAGGATGAGAAGATGATTCCTTCC 554
 QY 605 TTCAGGTGAAC 616
 Db 555 TTCAGACTTAAC 566

RESULT 3
 BUS49366/c
 LOCUS GM880016A20B10 Gm-r1088 Glycine max cDNA clone Gm-r1088-5828 3',
 DEFINITION mRNA sequence.
 ACCESSION BUS49366
 VERSION BUS49366.1 GI:22932227
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 622)
 Vodkin,L., Shoemaker,R., Keim,P., Retzel,E., Khanna,A., Shealy,R.,
 Clough,S., Thibaud-Nissen,F., Coryell,V., Erpeliding,J., Raph,C.,
 Shoop,E., Stromvik,M., Schweitzer,P., Gong,G. and Liu,L.
 A Functional Genomics Program for Soybean (NSF 9872565) (2002)
 Unpublished (2002)
 Other_Ests: BG881784 corresponding to Gm-cl065-2970 (5')
 Contact: Vodkin, L.O., PI, A Functional Genomics Program for
 Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional
 Genomics

University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l-vodkin@uiuc.edu
 Insert Length: 622 Std Error: 0.00
 Plate: GM880016A20 row: B column: 10
 Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'
 High quality sequence stop: 622.

FEATURES
 source

1. .622
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1088-5828"
 /clone_lib="Gm-r1088"

/note="The library Gm-r1088 is a sequence-driven, reracked
 set of 9,216 low redundancy clones selected from cDNA
 libraries from various tissues and stages of development
 of soybean that consists of 2,706 cDNAs from germinating
 cotyledons (source library Gm-cl027); 1,355 cDNAs from

immature seed coats (libraries Gm-cl019 and Gm-cl023); 917
 cDNAs from tissue culture derived somatic embryo8 (source
 libraries Gm-cl036 and Gm-cl075); 3,275 cDNAs from
 germinating seedlings, shoot tips, or leaves exposed to
 various stresses (source libraries Gm-cl064, Gm-cl065,
 Gm-cl066, and Gm-cl067; and Gm-cl068); and 963 cDNAs from
 young leaves exposed to bacterial and fungal pathogens
 (source libraries Gm-cl072, Gm-cl073, and Gm-cl074). The
 5' ESTs of the source clones from the different libraries
 was used to select singletons, or a representative of each
 contig, which were reracked to form library Gm-r1088 and
 the cDNA clones of the reracked Gm-r1088 library were then
 sequenced at the 3' end. The unigene selection and 3'
 sequencing was funded by NSF Plant Genome project #9872565
 (http://soybean.genomics.croptci.uiuc.edu/) as part of
 creation of a low redundancy soybean cDNA set. The source
 cDNA libraries were constructed by the laboratories of
 Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa
 State University, and Paul Keim, Northern Arizona
 University as part of the Public EST project,
 http://129.186.26.94/soybeanest.html. The contig analysis
 to select unique genes was performed by the laboratory of
 Ernest Retzel, Center for Computational Genomics and
 Bioinformatics, University of Minnesota,
 http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and 3'
 sequencing were conducted by services of the University of
 Illinois Keck Center for Comparative and Functional
 Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The
 corresponding 5' EST from each clone in the Gm-r1088
 library is listed in the 'OTHER EST' field. The detailed
 information on the source library for each clone can also
 be obtained by referring to the Genome Systems clone ID of
 the original cDNA library that is also listed under 'OTHER
 EST'."

ORIGIN

Query Match 32.6%; Score 430; DB 5; Length 622;
 Best Local Similarity 84.1%; Pred. No. 4.9e-104;
 Matches 522; Conservative 0; Mismatches 88; Indels 11; Gaps 3;
 QY 554 CAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGATTGCGCTTCAGGTG 613
 Db 621 CAGAGGAATGCTTGAGTAGGTTGCTGAAGGATGAGAGAGTGATCTTCCTCAGACTT 562
 QY 614 AACCACTACCGCCCTTGCCCTGAGGTGCAAGCACTGAA---CCGGAATTTGGTGGTTT 670
 Db 561 AACCNNAACCCGCCCATGCCAGAGGTGCAAGCATTGAACGGCAGAAATTTGGTGGTTT 502
 QY 671 GGGGAGCAGACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTG 730
 Db 501 GGAGAGCACACAGACCCACAGATAATTTCTGTCTTTGAGATCTTAACAGCACCTCAGGCCTG 442
 QY 731 CAATCTGCTCACAGATGGCAGCTTGGGTTTCAGTCCACCTGATCAGACTTCTCTTTTC 790
 Db 441 CAATCTGCTCACAGATGGCAGCTTGGGTTTCAGTCCACCTGATCAAACTTCTCTTTTC 382
 QY 791 ATCAATGTTGGTGAAGCTCTACAGGTAATGACTAATGGAGGTTTAAAGTGTAAAGCAT 850
 Db 381 ATCAATGTTGGTGAAGCTCTACAGGTAATGACTAATGGAGGTTTAAAGTGTAAAGCAT 322
 QY 851 AGGGTTTGGCTGACACAAAGCAAGTCAAGTTATCAATGATCTACTTTGGAGGACCCAGG 910
 Db 321 AGAGTTTGGCTGACCCCAACCAAGTCAAGTTGTCAATGATCTACTTTGGAGGACCC 262
 QY 911 TTGAGTGAATATAGCACCTTTTACCTTCAGTGATGTTTAAAGGAGAGAGGTTTGTAC 970
 Db 261 TTGAGTGAATATAGCACCTTTTACCTTCAGTGATGTTTAAAGGAGAGAGGTTTGTAC 202
 QY 971 AAAGATGTTCAATGTTGTGAATACAAAGGCTGGGTACACTTCAAGGCTAGCTGATAAT 1030
 Db 201 AAAGATGTTCAATGTTGTGAATACAAAGGCTGGGTATCGCTCAAGGCTAGCGGATAAT 142
 QY 1031 AGGCTTGGCCCTTTCCAGAAATCTGCTGTGATTAACCAAAACACACCCCTTCAAA-----T 1085


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||||| 141 AGGCTCGCTCCCTTTTGGAGAAATCTGCTGATTAAGAGATCCAAAGTGCTCAAAATTTT 82
||||| 1086 TCCACTCATTTTACGAGCGTGTATTACCCCAATTTT---CTTCTCTTTTCTTTTCCG 1142
||||| 81 ACTGCTCAATTTTGGCAGCGTATTGTTAGGGAACCTTTTTCATATATATATATATTTTGG 22
||||| 1143 TGTCTCTCTAGGTTTCAACA 1163
||||| 21 TTGTATCTAGGTTTCAACA 1

CNSOAC6N 1365 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB7ZE01 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).
BX814544
HTC; GSLT cDNA.
GI:42472102
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruado,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 1365)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen)
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_Full
_length
http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.
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1. .1365
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/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTFB7ZE01"
/tissue_type="Flowers and buds"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
1. .1365
/gene="Atlg30040"

gene
1. .1365
/gene="Atlg30040"

ORIGIN
Query Match 32.4%; Score 427.4; DB 4; Length 1365;
Best Local Similarity 66.4%; Pred. No. 2.9e-103;
Matches 630; Conservative 0; Mismatches 316; Indels 3; Gaps 1;

QY 146 ATTCTGTGTGACCTCAGCACCGACCCGATGCCAAGATCTCATAGTGAACCGCTGTAGG 205
||| 195 ATCCCCGTGCTCAACCTAGCCGATCCGGAAGCGAAACCCGAATCGTAAAGCCTCGCAG 254
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QY 206 GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTTGAGTTAATGGCAATTTA 265
||| 255 GAGTTTCGGGTCTTCAAGGTCGTAAACCCAGCGAGTCCGACCCGAACTCATGACTCGTTA 314
QY 266 GAAAAAGAGGCGCTCAGGTTCTTTAAAAATCTAGTCCGAGAAAAGACAGAGCTGTGCC 325
||| 315 GAGCAGGAGGCTATTGGGCTTCTTCGGCTTCGCTCAGTCTCTTTAAAAACCGGGCGGTCCA 374
QY 326 CCGGACCTTTTCGGCTATGGTAGCAAGAGGATTGGCCCAACGGTGATGTCGGTTGGGTC 385
||| 375 CCTGAACCGTACGGTTATGGTAATAAACGGATTGGACCAACCGGTGACGTTGGTTGGATT 434
QY 386 GAATACCTCTCTCAACCAACCAACCTGATGTATCTCAACCACCAATCACTTTGTCATTTTC 445
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QY 446 CGAGAAAAATCTCATCATTTTCAGGGCGGTGGTGGAGAACTACATTACAGCAGTGAAGAAC 505
||| 495 CGTCAAAACCCCTCAAAATTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 554
QY 506 ATGTGCTATGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 565
||| 555 GTGTCGTACAAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 614
QY 566 TTAAGCAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 625
||| 615 CTGAGTAAATCTCTGAGATGAGAGAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 674
QY 626 CTTGCGCTGAGTGCAGCAGTGCAGCAGTGCAGCAGTGCAGCAGTGCAGCAGTGCAGCAGTGC 685
||| 675 GCG---GCGGAGGAAGAGGCGGAGAGAGTGTGTAAGTGGGCTTTGGGGAACACACAGAC 731
QY 686 CCACAGATAATTTCTGTCCTTAAGATCTAACACACACATCTGGCTTGCATCTGTCTCACA 745
||| 732 CCACAGATAATCTCAGTGTCTAAGATCTAATAACACCGCGGGTCTTCAATCTGTGTGAAA 791
QY 746 GATGCACTTTGGTTCAGTCCCTCAGTCATCAGATCTCTCTTTTTCATCAATGTTGTGTGAC 805
||| 792 GATGGAAGTTGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 851
QY 806 GCTCTACAGGTAATCACTAATCGGAGTTTAAAGTGTAAAGCATAGGCTTTTGGCTGAC 865
||| 852 GCTCTTCAAGTATGACTAAACGGAGGTTCAAGAGTGTAAACACACAGGCTCTTAGCCGAT 911
QY 866 ACACGAAGTCAAGTTATCAATGATCTACTTTGAGGACCGAGCTGTGATGAAATATA 925
||| 912 ACAAGGAGATCGAGGATTTCAATGATATATTTTCGCGGACCGCCATTGAGCCAGAGATC 971
QY 926 GCACCTTTTACCTTCAGTGATGTAAAGGAGAGGAGTGTTCGTACAAAGAGTTTCACATCG 985
||| 972 GCACCATTCGCAATGCTTGTCCCTGAGCAGATGATTTGCTTTACAAAGATTCACATTCG 1031
QY 986 TGTGAATACAAGAGGCTCGGTACACTTCAAGGCTAGCTGATGAATAGGCTTCCCTCTTC 1045
||| 1032 TCTCAATCAAAATCTTCTGCTTACAAGTCTAAGCTTGGTGTATATAGACTTGGTCTCTTT 1091
QY 1046 CAGAAATCTGCTGCTGATTAACCAACACACCCCTTCAATTCACATTCATCAT 1094
||| 1092 GAGAAACCACTCTTGTCAATCATAAACCCCTTGTATGAGAGTAGTGCAT 1140

RESULT 5
CNSOABSJ 1362 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB7ZE01 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).
BX816963
HTC; GSLT cDNA.
GI:42471779
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
ORGANISM
```


QY	146	ATTCCTGTGGTCGACCTCAACGCCCGATGCCAAGAAATCTCATAGTGAACCCCTGTAGG	205
Db	193	ATCCCCGTCGTCACCTAGCCGATCCGAAGCGAAACCCGAATCGTAAAGCCCTGTAG	252
QY	206	GACTTGGGCTCTTCAAGCTGTGAACCAATGTTCCATGGAGTTAATGCCCAATTTA	265
Db	253	GAGTTGGGCTCTTCAAGCTGTGAACCAATGTTCCATGGAGTTAATGCCCAATTTA	312
QY	266	GAAACGAGGCGCTCAGGTTCTTTAAATAATCTCAGTCGAGAAACAGACAGCTGTC	325
Db	313	GAGCAGAGGCTATTGGCTCTTTCGGCTGCTCAGTCTCTTAAACCGGCGCTTCA	372
QY	326	CCGACCCCTTTCGGCTATGTTAGCAAGAGATTGGCCCAACCGGTGATGTCGGTTC	385
Db	373	CCTGAACCGTACGGTTATGTTAATAAACCGATTGCAACCAACCGGTGATGTCGGT	432
QY	386	GAATACCTCTCTCAACACCAACCTGATGTTATCTCACCCAAATCACTTTGCAATTT	445
Db	433	TAGTATCTCTCTCAATGCTAATCTCAGCTCTCTCTCTTAAACCTCCGCCGTTTC	492
QY	446	CGAGAAATCTCATCATTTTCAAGGCGGTGGGAGAACTACATTACAGCAGTGAAGAC	505
Db	493	CGTCAACCCCTCAATTTTCGCTGAGTTGGTGGAGGATACATGAGAGATTAGGAA	552
QY	506	ATGCTGATGCGGTGTGGAATTGATGCGGAGGGTTGGGATAGGCGAGGAAATACG	565
Db	553	GTTTCGTCAAGGTGTGGAGATGCTTCCGGAAGAACTAGGATAGAGCCAAAGGACACT	612
QY	566	TTAAGCAGGTTCTGAGGATGAGAAAGTATGTTGCTGCTCAGTTGACCACTACCG	625
Db	613	CTGAGTAAATCTCAGAGATGAGAGATGATGCTGCTGAGACTAATCAATTTATCCG	672
QY	626	CCTTCCCTGAGTGAACGACTGAACCGAATTTGGTTGGGTTGGGAGCACACAGAC	685
Db	673	GGG---GGGAGAGAGCGGAGAGATGTTGAGGTGGGTTGGGAAACACACAAAC	729
QY	686	CCACAGATAATTTCTCTTAAGATCTAACAGCACATCTGGCTGCAATCTGCTCA	745
Db	730	CCACAAATAATCTCAGTTCTAAGATCTAATAACACCGCGGGTCTTCAATCTGTGAA	789
QY	746	GATGCACTTGGTTCAGTCCCACTGATCAGACTCTCTTTTTCATCATGTTGGTAC	805
Db	790	GATGAAGTTGGGTGCTGCTCCTGCTGATCACTCTCTCTTCTTCAATTAATGGAGAT	849
QY	806	GCTCTACAGTAAATGACTAATGAGGTTTAAAGTGAAGCATAGGTTTGGCTGAC	865
Db	850	GCTCTTCAAGTTATGACTAACCGGAGTTTCAAGAGTTTAAACACAGGCTCTTACCGAT	909
QY	866	ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAAGCGTTGAGTGAAATATA	925
Db	910	ACAAGGAGATCGAGGATTTCAATGATATATTTTCGGCGGACCGCATTTGAGCCAGAATC	969
QY	926	GCACCTTTACCTTCAAGTATGTTAAAGAGAGAGGAGTGTGTTACAAAGATTCAATGG	985
Db	970	GCACCAATGCCATGCTGCTCCCTGAGCAAGATGATTTGGCTTTTACAAAGAAATCACTGG	1029
QY	986	TCGTAATCAAGAGGCTCGTACACTTCAAGGCTAGCTGATAATAGGCTTCCGCTTTC	1045
Db	1030	TCTCAATCAAAATCTTCTGCTTCAAGTCTAAGCTTGGTGGATATAGACTTGGTCTCTTT	1089
QY	1046	CAGAAATCTGCTGCTGATTAAACCAACACACCCCTTCAAAATCCACTCAT	1094
Db	1090	GAGAAACACCTCTCTTCAATCATATAAACCCCTTGTATGAGAGTAGTCAAT	1138

RESULT 8
 Locus: CNSOAC3R
 DEFINITION: Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSU7FB70ZF11 of flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
 ACCESSION: BX814383

VERSION	<p> BX814383.1 GI:42472054 HTC; GSLT cDNA. Arabidopsis thaliana (thale cress) Arabidopsis thaliana Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi. 1 (bases 1 to 1339) Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpetti, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M. Whole Genome Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation 2 (bases 1 to 1339) Genoscope. Direct Submission Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., URV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length http://www.genoscope.cns.fr/cgi-bin/ggb?ggb?source=Arabidopsis. Location/Qualifiers 1..1339 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /clone="GSLT7B70ZF11" /tissue_type="Flowers and buds" /ecotype="Col-0" /plasmid="pCMVSPORT_6" 1..1339 /gene="At1g30040" </p>
FEATURES	<p> source 1..1339 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /clone="GSLT7B70ZF11" /tissue_type="Flowers and buds" /ecotype="Col-0" /plasmid="pCMVSPORT_6" 1..1339 /gene="At1g30040" </p>
ORIGIN	<p> Query Match 29.3%; Score 386.4; DB 4; Length 1339; Best Local Similarity 66.9%; Pred. No. 3e-92; Matches 581; Conservative 0; Mismatches 281; Indels 6; Gaps 2; QY 146 ATTCCTGTGGTCGACCTCAACGCCCGATGCCAAGAAATCTCATAGTGAACCCCTGTAGG 205 Db 193 ATCCCCGTCGTCACCTAGCCGATCCGAAGCGAAACCCGAATCGTAAAGCCCTGTAG 252 QY 206 GACTTGGGCTCTTCAAGCTGTGAACCAATGTTCCATGGAGTTAATGCCCAATTTA 265 Db 253 GAGTTGGGCTCTTCAAGCTGTGAACCAATGTTCCATGGAGTTAATGCCCAATTTA 312 QY 266 GAAACGAGGCGCTCAGGTTCTTTAAATAATCTCAGTCGAGAAACAGACAGCTGTC 325 Db 313 GAGCAGAGGCTATTGGCTCTTTCGGCTGCTCAGTCTCTTAAACCGGCGCTTCA 372 QY 326 CCGACCCCTTTCGGCTATGTTAGCAAGAGATTGGCCCAACCGGTGATGTCGGTTC 385 Db 373 CCTGAACCGTACGGTTATGTTAATAAACCGATTGCAACCAACCGGTGATGTCGGT 432 QY 386 GAATACCTCTCTCAACACCAACCTGATGTTATCTCACCCAAATCACTTTGCAATTT 445 Db 433 TAGTATCTCTCTCAATGCTAATCTCAGCTCTCTCTCTTAAACCTCCGCCGTTTC 492 QY 446 CGAGAAATCTCATCATTTTCAAGGCGGTGGGAGAACTACATTACAGCAGTGAAGAC 505 </p>

Db	493	CGTCAAAACCCCTCAAAATTTTCCTGAGTCCGTTGAGAGGTACATGAAGAGAGATTAAAGAA	552
QY	506	ATGTGCTATGCGGTGTGGAATGTATGCGGAGGGTTGCGGATAGGACAGGAGATACG	565
Db	553	GTGTCTACAGGTGTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCAAGGGACACT	612
QY	566	TTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTTCAGGTTGAACCACTACCCG	625
Db	613	CTGAGTAAATGCTGAGAGATGAGAAGAGTGACTCGTGGCTGAGACTAAACCATTTATCCG	672
QY	626	CCTTGCCCTGAGGTGAAGACTGAACCGGAATTTGGTTGGGTTTGGGGAGCACACAGAC	685
Db	673	GC---GSCGAGGAGAGGCGGAGAGATGTTGAAGTGGGGTTTGGGGAAACACACAGAC	729
QY	686	CCACAGATAATTTCTGCTTAAGATCTAACAGCACATCTGGCTTGCAAAATCTGCTCACA	745
Db	730	CCACAGATAATCTCAGTGTAGATCTAATAACACGGCGGGTCTTCAAATCTGTGTGAAA	789
QY	746	GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTTTTCATCAATGTTGGTGAC	805
Db	790	GATGGAAGTTGGTGGCTGTCCCTCCTGATCACTCTTCTTCTTCAATTAATGTTGGAGAT	849
QY	806	GCTCTACAGTAAATGACTAATGGAGGTTTAAAGTGTAAAGCATAGGGTTTGGCTGAC	865
Db	850	GCTCTTCAGGTTATGACTAAACGGGGGTTCAAGAGTGTAAACACACAGGGTCTTAGCCGAT	909
QY	866	ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAAGCGTTGAGTGAATAATA	925
Db	910	ACAGGAGATCGAGGAATTTCAATGATATATTTTCGGCGGACCGCCATGTAGCCAGAAGATC	969
QY	926	GCACCTTTTACCTT---CAGTGTATGTTTAAAGGAGGAGGTGTTTGTACAAAGAGTTTACA	982
Db	970	GCACCAATTGCCATTGCTTGTCCCTGAGCAAGATGATTTGTGCTTTACAAAGAAATTCAC	1029
QY	983	TGTTGTGAATACAAAGAGCGTGGTTACA	1010
Db	1030	TGTTCTCAATACAAATCTTCTGCTTACA	1057
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DEFINITION	sr46c09.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1051-1097 5' similar to TR:064692 O64692 PUTATIVE GA4 PROTEIN. ; mRNA sequence.		
ACCESSION	BE802903		
VERSION	BE802903.1	GI:10234015	
KEYWORDS	EST.		
SOURCE	Glycine max (soybean)		
ORGANISM	Glycine max		
REFERENCE	1 (bases 1 to 612) Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvett, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Septoe, M., Theising, B., Allen, M., Bowers, J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Public Soybean EST Project Unpublished (1999)		
AUTHORS	Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD		
TITLE	Public Soybean EST Project		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD		
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)	High quality sequence stop: 413.		
FEATURES	Location/Qualifiers		
Source	1..612		
	/organism="Glycine max"		
	/mol_type="mRNA"		
	/cultivar="Corolla"		
	/db_xref="taxon:3847"		
	/clone="GENOME SYSTEMS CLONE ID: Gm-c1051-1097"		
	/tissue_type="floral meristematic mRNA"		
	/lab_host="DH10B"		
	/clone_lib="Gm-c1051"		
	XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dI) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."		
ORIGIN	Query Match 28.7%; Score 378.6; DB 2; Length 612; Best Local Similarity 88.4%; Pred. No. 3.2e-90; Matches 411; Conservative 0; Mismatches 54; Indels 0; Gaps 0;		
QY	65	ACCATGTTGTTCTGTCTCAGCCAGCATTGAACCCAGTTTTTCTCTTGTGAAACCATTTCAAG	124
Db	148	ACCATGTTGTTCTGTCTCAGCCAGCATTAAACCCAGTTTTTCTCTTGTGAAACCATTTCAAG	207
QY	125	TCACGCCCTTGTTCACGGGGATTCCTGTGGTGCAGCTCAGCACCCCATGCGAAGAT	184
Db	208	CCCACGCCCTTGTTCGGGGGATTCCTGTGGTGCAGCTCAGCACCCCATGCGAAGAT	267
QY	185	CTCATAGTGAACGCGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTCCA	244
Db	268	CACATAGTCNATGCTTCGAGGACTTCGGCTTCTTCAAGCTCGTGNACCAACCGTGTCCG	327
QY	245	TTGGAGTTAATGCGCAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCC	304
Db	328	TTACAGTTTCATGCGCAATTTTGGAAAAGAAACCCCTCGGGTTCTTCAAAAAACCTCAATCC	387
QY	305	GAGAAAGACAGAGCTGCTCCCGGCCCTTCGGCTATGGTAGCAGAGGATTTGCCCA	364
Db	388	GAGAAAGACAGAGCTGCTCCCGGCCCTTCGGCTATGGTAGCAGAGGATTTGCCCT	447
QY	365	AACGGTATGTCGGTTGGTGCAATACCTCTCTCAACACCAACCCCTCATGTTATCTCA	424
Db	448	AACGGGATGTCGGTTGGTGCAATACCTCTCTCAACACCAACCCCTCATGTTATCTCC	507
QY	425	CCCAATCACTTTGCAATTTCCGAGAAAATCTCATATTTCAGGCGGTGTGGGAAC	484
Db	508	CCCAAGTCACAGTTCATTTTCAGAGAAACGCTCTCAGAAATTCATGGCGGTGGGAGAA	567
QY	485	TACATTACAGCAGTGAAGAACATGTCTATGCGGTGTGGAAATTG	529
Db	568	TACATTAGAGCGGTGAACACATGTGCTATGACGTGGTGGAAATTG	612
RESULT 10			
LOCUS	AJ803092	785 bp mRNA linear	EST 08-DEC-2004
DEFINITION	AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018 5 05 018, mRNA sequence.		
ACCESSION	AJ803092		
VERSION	AJ803092.1	GI:51118420	
KEYWORDS	EST.		
SOURCE	Antirrhinum majus (snapdragon)		
ORGANISM	Antirrhinum majus		

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.

1 (bases 1 to 785)

Bey M., Stueber K., Fellenberg K., Schwarz-Sommer Z., Sommer H.,

Saedler H. and Zachgo S.

Characterization of Antirrhinum Petal Development and

Identification of Target Genes of the Class B MADS Box Gene

DEFICIENS

Plant Cell 16 (12), 3197-3215 (2004)

15539471

Contact: Schwarz-Sommer Z

Molekulare Pflanzengenetik

MPI fuer Zuechtungsforschung

Carl-von-Linne Weg 10, D-50829, Germany.

Location/Qualifiers

1..785

/organism="Antirrhinum majus"

/mol_type="mRNA"

/db_xref="taxon:4151"

/clone="018.5.05.018"

/tissue_type="whole plant"

/clone_lib="Antirrhinum majus whole plant"

ORIGIN

Query Match 27.0%; Score 355.8; DB 1; Length 785;

Best Local Similarity 68.4%; Pred. No. 4.5e-84;

Matches 508; Conservative 0; Mismatches 232; Indels 3; Gaps 1;

302 TCCGAGAAAGACAGAGCTGGTCCCCCGACCCCTTTCGGCTATGGTAGCAAGAGGATTGGC 361

20 TCTGAAAAGGAGAAACAGGGACCCCTGACCCCTTTTGGCTATGGAAGTAAGAAAATTGGA 79

362 CCABAAGGTGATCGGTGGTTCGAATACCTCCCTCAACACCAACCTGATGTATC 421

80 CCATATGGGATGTGGGATGGGTGGAATACCTTTCCTTAACACATTAATCTGATCTGAT 139

422 TCACCAAAATCACTTTGCAATTTCCGAGAAAATCTCTCATCTTCAGGCGGTGGAG 481

140 TACAGAAATTTCATCGTGTGGTGAAGCTGCAGAAAATTCAGGTGTATGTAAT 199

482 AACTACATPACAGCTGGAAGAACATGTCTATGCGGTGTGGAATGATGCGAGGGG 541

200 GATTATGTTCTGCAGTAAAGAAATGGCGTGTGAGATCTTGAAATGTGCTGATGAA 259

542 TTGGGGATPAGCAGAGGATACCTTAACAGGTTGCTGAAGGATGAGAAAGTCAATCG 601

260 CTTAAGATTCACAAAGGAAACGCTTTTAGCAAACTTTTAATGGATGAACAGAGTGACTCT 319

602 TGCTTCAGGTTCAACCACTACCCGCTTCGCCCTGAGGTGCAAGCACTGAACCGAATTG 661

320 GTTTTCAGCTTAATCACTATCCATGCCCGGAATTCAGAAATCCAACT---ACTTA 376

662 GTTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACA 721

377 ATCGGTTTGTGGAACATACCTGACCCGCAAAATATATCGTTTTCAGATCCCAACACT 436

722 TCTGGCTGCAAACTGTCTCAGATGCACTTGGGTTTTCAGTCCACCTGATCAGACT 781

437 TCGGGTCTTCAAATTTTCGTTGAAAGATGGGAATTTGATTTCTATCCCACTGATCAAAAT 496

782 TCCTTTTTCATCAATGTTGGTCAAGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGT 841

497 TCTTTCTTCAATTAATGTTGGTCACTACGAGGTTATGACTAATGGCAGGTTTAAAGT 556

842 GTAAGACATAGGTTTGGCTGACACCAACGAAAGTCAAGGTTATCAATGATCTACTTTTGA 901

557 GTAAGACACAGGGTGTGCGCAACAGCTCAAAACCAAGACTTTCAATGATATATTTTGA 616

902 GGACCAAGCGTTGAGTGAATAATAGCACCTTTTACCTTCAGTGTATTTAAAGAGAGGAG 961

617 GGACCAACCAATTAAGTGAAGAATAGTCTCCATTTGCCTTTCAGTACTAATGAAGAGAGAC 676

QY 962 TGTTTGTACAAGAGCTTCACATGGTGTGAATACAAGAGGCTGCCTACACTTCAAGGCTA 1021

Db 677 AGCTTGTACAAGGAATTTACTTGTGTTGAGTACAAAAAATCTGCTTATAATCAAGGCTGG 736

QY 1022 GCTGATATAGCTTGCCTTTT 1044

Db 737 GCTGATAATAGTGGTCTGTTT 759

RESULT 11

CNSOADM

LOCUS

DEFINITION

Arabidopsis thaliana Full-length cDNA Complete sequence from clone

GSUTFB56ZG10 of Flowers and buds of strain col-0 of Arabidopsis

thaliana (thale cress).

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen)

full-length libraries construction : Temple G

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

URV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

genome released by MIPS (Munich Information center for Protein

Sequences). 5 prime and 3 prime are assembled with Phrap.

length

http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.

Location/Qualifiers

1..1128

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/clone="GSUTFB56ZG10"

/tissue_type="Flowers and buds"

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complement(1..1128)

/gene="At1g78440"

gene

ORIGIN

Query Match 26.4%; Score 348.6; DB 4; Length 1128;

Best Local Similarity 62.7%; Pred. No. 4.2e-82;

Matches 581; Conservative 0; Mismatches 334; Indels 12; Gaps 2;

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QY 192 TGAACGCTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACCATGCTGTTCCATTGGAGT 251


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Db 144 TGAAGAGTCGGAAGACTTCGCGCTTCTCAAGGTGATCAACCATGCGCTTTCGCGAGAGC 203
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QY 312 ACAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTTAGCAAGAGGATGTCGCCCAAGCGTG 371
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Db 321 ACGTGGTTGGGTTCGATGACTTGTGATGAACGCTAATCATGATTCGCGTTCGGGTCCAC 380
QY 432 CACTTTGCAATTTCCGAGAAAATCCTCATCATTTTACGGCGGTGGTGGAGAACTACATTA 491
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QY 552 GGCAGAGGAATACGTTAAGCAGAGTGTCTGAAGGATGAGAAAAGTGAATTCGTCTCAGGT 611
Db 501 AACCGAGGAACACACTTAGCAAGCTGTATCTGACCAAAACACGGAATCGATATTGAGAC 560
QY 612 TGAACCACTACCGGCTTCGCTGAGGTGCGAGCACTGAAC-----CGGAATTTGG 662
Db 561 TTAATCACTATCCACCATGCTCTTTAGCAATAAGAAAACCAATGGTGTGAAGAATGTGA 620
QY 663 TTGGGTTTCGGGAGCACACAGACCCACAGATAATTTCTCTTAAGATCTTACACGACAT 722
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QY 843 TAAAGCATAGGTTTGGCTGACACAAACGAGTCAAGGTTATCAATGATCTACTTTGGAG 902
Db 801 TGAGGCATAGGTTTATGCTCACTGTAAAAAATCTAGGGTTTCTATCAITTTACTTCGCTG 860
QY 903 GACCAGCTGTGAGTGAATAATAGCACCTTTTACCTTCAGTGATGTTTAAAGGAGAGGAGT 962
Db 861 GACCTTCATTGACTCAGAGAAATCGCTCCGTTACATGTTTGTAGACAAATGAGGACGAG 920
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QY 1023 CTGATAATAGGCTGCGCCCTTTCCAGA 1049
Db 981 CTGATAATAGGCTTCAACAATTGAAA 1007

RESULT 12
BM893076
LOCUS
DEFINITION
Gm-c1069-2961 5', similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA
sequence.
ACCESSION
BM893076
VERSION
BM893076.1 GI:19348544
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
```

```
REFERENCE
AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
Location/Qualifiers
1. 567
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/cultivar="Williams"
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etiolated seedling"
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/clone_lib="Gm-c1069"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etiolated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."
```

Query Match 25.5%; Score 336.2; DB 3; Length 567;
Best Local Similarity 88.4%; Pred. No. 7.7e-79;
Matches 365; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 65 ACCATGTTGTTCTGTCTCAGCCAGCATTTGAACACCACTTTTCTCTCTGAAACCATTTCAAG 124
Db 154 ACAATGTTGTTTGTCTCAGCCAGCATTAACCACTTTTCTCTCTGAAACATGCAAG 213
QY 125 TCCAGCCCTTGTTCACGGGGATTCGTGTGTCGACCTCACGCACCCCGATGCCAAGAT 184
Db 214 CCCAGCCCTCTTCTCCGGGATTCCTGTTGTCGACCTCACGCACCCCGATGCCAAGACC 273
QY 185 CTCATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTCCA 244
Db 274 CACATAGTGAAGCCCTGCGAGGACTTCGGCTTCTTCAAGCTCGTGAACCAACCGGTGTCCA 333
QY 245 TTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304
Db 334 TTAGAGTTTCATGCCCAATTTGAAAACGAAACCTCAGGTTCTTCAAAAACCTCAGTCC 393
QY 305 GAGAAAGACAGAGCTGGTCCCCCGACCTTTTGGCTATGGTAGCAAGAGGATTTGCCCA 364
Db 394 GACAAAGACAGGCTGGTCCCTCTGATCCTTTTGGCTAGCGCAGCAAGAGGATTTGCCCT 453

ORIGIN

ORIGIN	Query Match	25.4%;	Score 335.4;	DB 2;	Length 694;
	Best Local Similarity	69.6%;	Pred. No. 1.3e-78;		
	Matches 485;	Conservative	0;	Mismatches 206;	Indels 6; Gaps 2;
QY	336	TCGCGTATGTTAGCAAGAGATTGGCCCAACGGTGTATGTCGGTTGGTTCGAATACCTCC	395		
DB	1	TTGGTTATGGCAATAGAGAAATCGGACAAATGGCGATATCGGTGGTGGATACATTC	60		
QY	396	TCCTCAACCAACCCCTGATGTTATCTCA CCGCAATCACTTTGCATTTCCGAGAAATC	455		
DB	61	TCCTTTTCAACAAATTTCTGAAATTCAAATTACCAGAAATTCGCATCTGTATTAGGTGTC	120		
QY	456	CTCATCATTTTCAGGCGGCTGGTGAGAACTACATTTACAGCAGTCAAGAACATGTGCTATG	515		
DB	121	CAGAAACATTCGGGCTCGGTGNAATGATATGTGTCTATCGTGAAGAAATGTCTATGTG	180		
QY	516	CGGTGTTGGAATTGATCGCGAGGGGTTGGGGATTAAGCGCAGAGAAATACGTTAAGCAGGT	575		
DB	181	AGATTCCTTGAAAGTTTCGGCGAGGGATTAAGAATTCAACCCAGCAATGTTTTCAGTAGAC	240		

QY	576	TGCTGAAGATGAGAAAAGTGATTCTGTGCTTCAAGTTTGAACACACTACCCGCTTGCCTTG	635
Db	241	TATTGTGATGAGAAAGAGCGGACTCTGTGTTTTCAGGCTGAATCACTATCTCTCCATGTGCTTG	300
QY	636	AGGTGCAAGCAGCTGAA--CCGGAATTTGGTTTGGGTTTGGGAGACACAGACCCACAGA	692
Db	301	ATATTCAGAAATTCATGCGAAAAATTTAATTGGATTGGAGAACATCTATGATCCACAAA	360
QY	693	TAATTTCTGCTTTAAGATCTAAACAGACACATCTGGCTTGCAAAATCTGCTCTCACAGATGGCA	752
Db	361	TCATGTCGATTTTAAGATCCAAACACACCTCCGGCTCTCAAATTTTACTCAAAAATGGCA	420
QY	753	CTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTTTCAATCAATGTTGGTGAGGCTCTAC	812
Db	421	ACTGGTTTTCTGTTCCATCTGATCAGAAATCTCTTTTTCGTCAATGTTGGAGACTCAATTAC	480
QY	813	AGGTAATGACTAATGGAGGTTTAAAGTGTAAGCATAGGTTTGGCTTGACACAAACGA	872
Db	481	AGGTGATGACGAATGGAAGTTTAAAGATGTGAACATAGGTTGTTGACAAACAGTGTGA	540
QY	873	AGTCAAGGTTTATCAATGATCTACTTTGGAGGACCAGCGTTTGAGTGAAAAATATAGCACCTT	932
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QY	993	ACAAGAGGCTCGGTACACTTCAAGGCTAGCTGATAA	1029
Db	658	ACCAAAAGTCAGCTTACAGACTAGACTAGCTGATAA	694

RESULT 14

AL382874

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AL382874

MtBC10E02F1 MtBC Medicago truncatula cDNA clone MtBC10E02 T3, mRNA sequence.

AL382874

AL382874.1 GI:9682625

EST.

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 478)

Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O., Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson,V. and Gamas,P.

Medicago truncatula ESTs from endomycorrhizal roots

Unpublished (2000)

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : Mt-est@toulouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mttruncatula.html).

FEATURES

source

1..478

/organism="Medicago truncatula"

/mol_type="mRNA"

/cultivar="Jemalong"

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/clone="MtBC10E02"

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/clone_lib="MtBC"

/notes="Vector: pBluescript pSK; Site 1: EcoRI; Site 2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C. before transplanting into a 1/3 Epsilones soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP48) . The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAseit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of fungal origin."

ORIGIN		Query Match	25.3%;	Score 332.8;	DB 1;	Length 478;
		Best Local Similarity	83.0%;	Pred. No. 6.1e-78;		
		Matches 395;	Conservative 0;	Mismatches 72;	Indels 9;	Gaps 1;
QY	557	AGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGATTGCGTTCAGGTTGAAC	616			
DB	3	AGAAATGTTAAGCAGGTTATTGAAGATGAGAAAGTGATTGTTTCAAAATTAAC	62			
QY	617	CACATCCCGCTTGCCTGAGGTGCAAGCA-----CTGAACCGGAATTTGGTTGGG	667			
DB	63	CATTACCCACCGTGCCTGAGGTGCAACAGCAGCATTTGAATGGAAGGAATTTGCTTGGG	122			
QY	668	TTTGGGGAGCACACACACCCACAGATAATTTCTGCTTAAGATCTTAACAGCACATCTGGC	727			
DB	123	TTTGGGGAGCATACAGACCCACCAAGTCATTTCTGCTTGAGATCTTAATAGCACATCAAGA	182			
QY	728	TTGCAAAATCTGCTCAGAGATGCACCTTGGGTTTCAAGTCCACCTCATCAGACTTCCTTT	787			
DB	183	CTGCAAAATCTGCTCAGATGAGAACTTGGGTTTCAAGTCCACCTCATCAGACTTCCTTT	242			
QY	788	TTCATCAATTTGGGTGACGCTCTACAGGTAATGACTTAATGGGAGGTTTAAAGTGTAAG	847			
DB	243	TTCATCAATTTGGGTGATACCTTTCAGGTATTGACTTAATGGTGGTAAAGTGTAAG	302			
QY	848	CATAGGTTTGGCTGACACCAACGAGTCAAGTTATCAATGATCTACTTTGGAGGACCA	907			
DB	303	CATAGGTTTGGCTGACACCAACAAAGTCAAGTTGTCGATGATATACCTTTGGAGGACCA	362			
QY	908	GCCTTCAGTGAAATATAGCACCTTTTACCTTCAGTGTATGTTAAAGGAGGAGTGTTG	967			
DB	363	CCCTTGAGTGAAAGATAGTGCCTTTTACCTTCTTTAATGTTAAAGAGAGAAAGTTTG	422			
QY	968	TACAAAGAGTTTCATGGTGTGAATACAAAGAGGCTCGGTACACTTCAAGGCTAGC	1023			
DB	423	TACAAAGAGTTTACGTTGGTGGAGTACAAGAAAGCAATGTACAATTTCAAGGCTGGC	478			

RESULT 15
DN589159
LOCUS
DEFINITION
50141.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
50141.5', mRNA sequence.
DN589159
ACCESSION
DN589159.1 GI:61239615
VERSION
KEYWORDS
SOURCE
Solanum tuberosum (potato)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 893)
REFERENCE
Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De

TITLE
JOURNAL
COMMENT

Koeber,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@biatlantech.nb.ca
Seq primer: T3.

FEATURES
source

1..893
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="50141"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Query Match	25.0%;	Score 329.2;	DB 8;	Length 893;
Best Local Similarity	67.6%;	Pred. No. 6.5e-77;		
Matches 495;	Conservative 0;	Mismatches 228;	Indels 9;	Gaps 2;
329	GACCCCTTCGCGTATGTTAGCAGAGGATTTGCCCAACGGTGATGTCGGTTGGGTCGAA	388		
3	GACCCCTTCGCGTATGTTAGCAGAGGATTTGCCCAACGGTGATGTCGGTTGGGTCGAA	62		
389	TACCTCTCTCAACACCAACCCCTGATGTTATCTCAACCAATTCATTTGGCATTTTCCGA	448		
63	TACATCTCTTTGTCAACAAATTTCTGAGTTCAATTTACCAAAATTTTGCATCTATTTTGGGT	122		
449	GAAATCTCTCATCATTTTCAGGGCGGTGGTGAGAACTACATTACAGCAGTGAGAACATG	508		
123	GTCAATCCAAAAGATATAAGAGATGCTGTGAATGATTTATGTATTAGCAATGAAGAAAAATG	182		
509	TGCTATGCGGTGTTGGAATTTGATGGCGAGGGGTTGGGGATAAGGCAGAGAAATACGTTA	568		
183	GCTTGAGATCTTTGAAATGTTAGCAGAGGGATTTAAAAATTCATCCAAGAAATGTTATT	242		
569	AGCAGGTTGCTGAAGGATGAGAAAAGTGTATTCGTGCTTCAGGTTGAACCACTACCCGGCT	628		
243	AGTAAGCTTTTAAATGGATGAAAAAAGTGATTCACCTTTTAGCTAAATCATTTACCCTCCA	302		
629	TGCCCTGAGG-----TGCAAGCAGCTGAACGGGAATTTGGTTGGGTTGGGGAGCACACA	682		
303	TGTCCTGATGAATTTCAAGAAATATAATGGAAGAAATTTAAATTTGGATTTGGTGAACATCT	362		
683	GACCCACAGATAATTTCTGCTTTAAGATCTTAACAGCAGCATCTGGCTTGCAAAATCTGTCTC	742		
363	GATCCACAAATTAATTTCTTTTAAAGATCCAAATAACACTCTCTGGACTTCAAATTTCACTT	422		
743	ACAGATGGCACTTGGGTTTTCAGTCCACCTGATCAGACTTCTTTTTCATCAATGTTGGT	802		
423	GTTGATGGCCATTTGGATTTCTGTCCCACTGATCAAAATTCATTTCTTCATCAATGTTGGT	482		
803	GAGCGCTCTACAGGTTAATGACTTAATGGGAGGTTTAAAGTGTTAAAGCATAGGTTTGGCT	862		
483	GATTCAATTGACAGGTGATGACAAAATGGGAGGTTTAAAGTGTTAAACATAGAGTTTGGCC	542		


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Qy      923 ATAGCACCTTTACCTTCAGTGATGTTAAAGGAG---AGGAGTGTGTTGTACAAAGAGTTC 979
Db      603 ATAGCACCAATTGTCATCACTATTAAATAAAGGGGATCAAGACAGCTTGTACAAAGAAATT 662
Qy      980 ACATGGTGTGAATACAAGAGGCTGCGTACACTTCAAGGCTAGCTGATATAATAGGCTTGCC 1039
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Qy      1040 CCTTCCAGAA 1051
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Job time : 6016.88 secs

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GenCore version 5.1.6
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Run on: December 27, 2005, 17:48:03 ; Search time 268.271 Seconds
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Title: US-10-670-454-1

Perfect score:

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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	1318	100.0	1318	3	US-09-719-108-1	Sequence 1, Appl	
2	893.8	67.8	1359	3	US-09-371-307-62	Sequence 62, Appl	
3	430.8	32.7	1352	3	US-09-614-912-13	Sequence 13, Appl	
4	429.2	32.6	1365	3	US-09-614-912-5	Sequence 5, Appl	
5	425.8	32.3	1237	3	US-09-719-108-7	Sequence 7, Appl	
6	424.8	32.2	1403	3	US-09-371-307-64	Sequence 64, Appl	
7	382.8	29.0	1008	3	US-09-719-108-9	Sequence 9, Appl	
8	363.6	27.6	1473	3	US-09-614-912-7	Sequence 7, Appl	
9	356.6	27.1	1318	3	US-09-719-108-5	Sequence 5, Appl	
10	354	26.9	1650	3	US-09-614-912-3	Sequence 3, Appl	
11	315.8	24.0	1555	3	US-09-614-912-1	Sequence 1, Appl	
12	311	23.6	783	3	US-09-371-307-67	Sequence 67, Appl	
13	166	12.6	811	3	US-09-371-307-71	Sequence 71, Appl	
14	155.6	11.8	403	3	US-09-371-307-66	Sequence 66, Appl	
15	154.8	11.7	406	3	US-09-371-307-68	Sequence 68, Appl	
16	152.4	11.6	966	3	US-09-371-307-58	Sequence 58, Appl	
17	120	9.1	426	3	US-09-371-307-70	Sequence 70, Appl	
18	113.6	8.6	450	3	US-09-614-912-9	Sequence 9, Appl	
19	103	7.8	210	3	US-09-719-108-3	Sequence 3, Appl	
20	101	7.7	199	3	US-09-719-108-4	Sequence 4, Appl	
21	80	6.1	595	3	US-09-614-912-15	Sequence 15, Appl	
22	75.8	5.8	618	3	US-09-614-912-11	Sequence 11, Appl	
23	72.4	5.5	723	3	US-09-371-307-56	Sequence 56, Appl	
24	72.4	5.5	4170	3	US-09-371-307-57	Sequence 57, Appl	

RESULT 1

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US-09-719-108-1
; Sequence 1, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberallin 2-Oxidase
; FILE REFERENCE: 0623-0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-09-719-108-1

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ALIGNMENTS

Sequence 1, Appli
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Db 1261 CCCTTTCCCTCAATTTGTCAATGGAAACGCACTCTAGTTTACAAAAAATAAAAAA 1318
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US-09-371-307-62
; Sequence 62, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-371-307-62
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Query Match 67.8%; Score 893.8; DB 3; Length 1359;
Best Local Similarity 84.9%; Pred. No. 1.5e-255;
Matches 1069; Conservative 1; Mismatches 158; Indels 31; Gaps 5;
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Qy 125 TCCACGCCCTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGCACCCCGATGCCAAGAT 184
Db 159 CCCACGCCCTTGTTCGCGGGGATTCCTGTGTGTCGACCTCAGCACCCCGATGCCAAGAC 218
Qy 185 CTCATAGTGAACGCCCTGTAGGGACTTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCCTCA 244
Db 219 CACATAGTCAATGCCCTGTGAGGACTTTCGGCTTCTTCAAGCTCGTGAACCATGTGTTCG 278
Qy 245 TTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCC 304
Db 279 TTACAGTTTCATGGCCAAATTTGGAACACGAAACCCCTCGGTTCTTCAAAAAACCTCAATCC 338
Qy 305 GAGAAAGACAGAGCTGGTCCCGGACCCCTTTCGGCTATGGTAGCAAGGATTTGCCCA 364
Db 339 GAGAAAGACAGAGCTGGTCCCGGACCCCTTTCGGCTATGGTAGCAAGGATTTGCCCT 398
Qy 365 AACGGTGATGTGGGTTGGGTGCAATACCTTCCTCCTCAACACCAACCCCTGATGTTATCTCA 424
Db 399 AACGGCGATGTGGGTTGGGTGCAATACCTTCCTCCTCAACACCAACCCCTGATGTTATCTCC 458
Qy 425 CCCAAATCATCTTTGCAATTTTCCGAGAAAATCTCATCATTTCAAGGCGGTGGTGGAGAAC 484
Db 459 CCCAAGTCAAGTTTCATTTTTCAGAGAAAGTCTCTCAGAAATTTTCAGGCGGTGGTGGAGAA 518
Qy 485 TACATTTACAGCAGTGAAGAACATGTCTATGCGGTGTGGAAATGATGCGGAGGGGTTG 544
Db 519 TACATTTAGAGCGGTGAAGAACATGTCTATGAGGTGTGGAAATGATGCTGAGGGATG 578
Qy 545 GGGATAAGGCAGAGGAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAATGATTTGTTGC 604
Db 579 GGGATAAGGCAGAGGAATGTTTGAAGTGTGCTGAAGGATGAGAAAGTGAATCTTGC 638
Qy 605 TTCAGGTTGAAACCACTTACCCGCTTTCGCTGAGGTGCAAGCACTGAAC---CGGAATTTG 661
Db 639 TTCAGACTTAAACCACTTACCCGCTTTCGCTGAGGTGCAAGCACTTGAACCGAAGAAATTTG 698
Qy 662 GTTGGGTTTGGGAGCACACAGACCACAGATAATTTCTGCTTAAAGATCTAACACACA 721
Db 699 GTTGGATTTGGAGAGCACACAGACCACAGATAATTTCTGCTTGTAGATCTAACACGACC 758
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QY 722 TCTGGCTTCCAAATCTGTCTCAGATGCGACTTGGGTTTTCAGTCCCACTGATCAGACT 781
Db 759 TCAGGCTTCCAAATCTGTCTCAGATGCGACTTGGGTTTTCAGTCCCACTGATCAGACT 818
QY 782 TCTTTTTCATCAATGTGGTGCAGCTCTACAGGTAACTAACTAACTGGGAGGTTTAAAGT 841
Db 819 TCTTTTTCATCAATGTGGTGCAGCTCTCTCAGGTAACTAACTAACTGGGAGGTTTAAAGT 878
QY 842 GTAAGCATAGGTTTGGCTGACACCAACGAAATCAAGGTATCAATGATCTACTTTTGA 901
Db 879 GTAAGCATAGGTTTGGCTGACACCAACGAAATCAAGGTATCAATGATCTACTTTTGA 938
QY 902 GGACGAGCTTGAATCAATATAGCACCTTTACCTTCACTGATGTAAAGGAGGAG 961
Db 939 GGACGAGCTTGTGTAAGATAGCACCTTTACCTTCACTGATGTAAAGGAGGAG 998
QY 962 TGTGTGTCAAGAGAGTTTCAATGTGTGAATCAAGAGGCTGCTACACTTCAAGGCTA 1021
Db 999 AGTTTCTCAAGAGAGTTTCAATGTGTGGGAATCAAGAGGCTGCTACAGGCTA 1058
QY 1022 GCTGATAATAGGTTTGGCTTCCAGAAATCTGCTGCTGATTAACCAACACACCCCTTC 1081
Db 1059 GCGGATAATAGGTTTGGCTTCCAGAAATCTGCTGCTGATTAAGGAGGCAAGTGCT 1118
QY 1082 AAA-----TTCACACTATTTAGGACGCTGTTATACCCAA-----TTTCTTCTCTTTT 1132
Db 1119 CAAAATTTCTACTACTCAATTTTGGCAGCTGTTGTTAGGCAACTTTTTTTATTTATTT 1178
QY 1133 TCTTTTCTGCTGCTGCTGATTTTCAACAGTGTGCTACTTCAATATATAGAAAT 1192
Db 1179 TTTTGGGTGTGTATCTAGGTTTCAACAGTGTGCTACTTCAATATATAGAAAT 1238
QY 1193 GAATAGT-----TAAGATGTTTATCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1241
Db 1239 GAATAGTGTCTATGCACTTCTTTTAACTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1298
QY 1242 TAAAGTGTGCTCAACTTCCCTTTCTCAATGTCAATGGAAGCACTCTAGTTACA 1300
Db 1299 TAAATGT-----CACTACTGCTTCTTATTAATCAATGAAACGCACTCTAGTCACA 1349
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RESULT 3

US-09-614-912-13

; Sequence 13, Application US/09614912

; Patent No. 6677502

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Rafalski, Antoni

; APPLICANT: Orozco, Buddy

; APPLICANT: Miao, Gou-Hau

; APPLICANT: Famodu, Omolayo O.

; APPLICANT: Lee, Jian Ming

; APPLICANT: Sakai, Hajime

; APPLICANT: Weng, Zude

; APPLICANT: Cai, Perry G

; APPLICANT: Anderson, Shawn

; TITLE OF INVENTION: Plant Metabolism Genes

; FILE REFERENCE: BB1378 US NA

; CURRENT APPLICATION NUMBER: US/09/614,912

; CURRENT FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: 60/143,401

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/143,412

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/146,650

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: 60/170,906

; PRIOR FILING DATE: 1999-12-15

; PRIOR APPLICATION NUMBER: 60/172,959

; PRIOR FILING DATE: 1999-12-21

; PRIOR APPLICATION NUMBER: 60/172,946

; PRIOR FILING DATE: 1999-12-21

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 13

; LENGTH: 1352

; TYPE: DNA

; ORGANISM: Glycine max

US-09-614-912-13

Query Match 32.7%; Score 430.8; DB 3; Length 1352;

Best Local Similarity 65.7%; Pred. No. 1.2e-117;

Matches 665; Conservative 0; Mismatches 332; Indels 15; Gaps 2;

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QY 55 AACAAACAACCACTGGTGTCTCTCAGCCAGCAATTAACCACTGTTTCTCTCTGAA 114
Db 146 AACAAACAAGAAAATGGTGTGTCTCAGCAACCAACAGAAACAATACTCTCAATTA 205
QY 115 ACCATTCAAGTCCAGCCCTTGTTCACGGGATTCCTGTGTGCGACCTCACGACCCCGA 174
Db 206 GAACCTGCATGCCAACCAAAATTTCTCAACAATTCCTCATAGTGGACCTCTCCAACTGA 265
QY 175 TGCAGAAGATCTCATAGTGAAGCCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACA 234
Db 266 TCAAAAGACCCCTTATAGTGAAGGCTTGTGAGGAGTTTGGATTTCTTCAAAAGTCATCAATCA 325
QY 235 TGGTGTTCATTTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAA 294
Db 326 TGGTGTCTCCATGGAAGCTATATCCGAATTTGGAATATGAAGCCTTCAAAATTTCTCTAT 385
QY 295 ATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCGCCACCTTTCCGCTATGGTAGCAAGAG 354
Db 386 GTCACCTCAATGAAAAGAAAAGTAGGACCTCCCAATCCATTTGGGTATGGTAGCAAGAA 445
QY 355 GATTGCCCAACCGGTGATGTGGTGGTGAATACCTCTCTCAACACCAACCCCTGA 414
Db 446 AATTGACACAAATGGGACGTTGGTGGATTTGAGTACCTTCTTCAACACCAATCAAGA 505
QY 415 TGTATCTCACCCTCAATCATTGTCATTTTCCGAGAAATCCCTCATCTATTTTCAGGGCGGT 474
Db 506 ACACAACCT-----TCTCTGTTTATGGGAAAAACCCCTGAGAAATTCAGGTGTCT 553
QY 475 GGTGAGAACTACATTACAGCAGTGAAGAAATGTGCTATGCGGTGTTGGAATTTGATGGC 534
Db 554 GTTGAACAGTTACATGTCTCTGTGAGGAGATGCGATGTGAGATTTCTGAGTTGATGGC 613
QY 535 GGAGGGTTGGGATTAAGCAGAGAGAAATCGTTAAGCAGGTTGCTGAAGGATGAGAAAAAG 594
Db 614 AGAAGGTTGAAGATTCAGCAAAAAGGATGTGTTAGCAAGCTTCTAAATGGATAAACAAAG 673
QY 595 TGATTCGTGCTTCAGGTTGAACCACTACCCGCTTCCCTGAGGTGCAAGCACTGNAACCG 654
Db 674 TGACTCTATTTTCAGGGTGAATCATTTACCTGCTTGTCTCTGAATGACTCTCTGAATGATCA 733
QY 655 GAATTTGGTGGTGGTGGGAGCACAGACCCACAGATAAATTTCTGCTTAAAGATCTAA 714
Db 734 GAACCTGATGGTGGTGGGAGAACACAGACCCACAAATCATCTCTCTGTTAAGATCCAA 793
QY 715 CAGCACATCTGGCTTCCAAATCTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGA 774
Db 794 CAACACTTCAGGCTTCCAGATTTATCTTTAGAGATGGAATTTGATTTTCACTCCCAACAGA 853
QY 775 TCAGACTTCTTTTTCATCAATGTTGGTGAAGCTCTACAGGTAATGACTTAATGGGAGGTT 834
Db 854 TGACAAATCTTTTTTATTAACGTTGGTGAATTTCTCTTCAAGGTTATGACAAATGGAAGGTT 913
QY 835 TAAAAAGTGTAAAGCATAGGTTTTCGCTGACACCAAGTCAAGGTTATCAATGATCTA 894
Db 914 CCGAAGTGTGAGACACAGAGTGTGGCAAAATGGGTTCAAGTCCAGGCTTCAATGATTTA 973
QY 895 CTTTGGAGGACAGCGTTGAGTGAATAATATAGCACCTTTTACCTTCAGTGAATGTTAAAAAG 954
Db 974 CTTTGGAGGTCACCTTTGAGTGAGAAAAATAGCACCAATTTATCTCTCTCATG---AAAGG 1030
QY 955 AGAGGAGTGTGTTATCAAAAGAGTTTCACTGTTGTAATCAAGAGGCTGCGTACACTTC 1014
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Db 1031 AAAAGAAAGCTATATAAAGAGTTTACCTGGTTTGAGTACAAAAAATCAATCTACGGTTC 1090
QY 1015 AAGGCTAGCTGATATAGGTTGCCCTTTTCGAGAAATCTGCTGTGATTAA 1066
Db 1091 AAGATTATCTAAAAATAGACTTTGAACATTTTGAAGAATTCGAGCTTCGTAA 1142
RESULT 4
US-09-614-912-5
; Sequence 5, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Calimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-5

Query Match 32.6%; Score 429.2; DB 3; Length 1365;
Best Local Similarity 65.6%; Pred. No. 3.7e-117;
Matches 664; Conservative 0; Mismatches 333; Indels 15; Gaps 2;
QY 55 AACAAACACACCATGGTTGTTCTGTCTCAGCCAGCATTTGAACAGTTTTCCTTCTGAA 114
Db 153 AACAAACAGAAAATGGTTGTTGTCTCCAAAGCAACACAGAAATATCTCTACATTA 212
QY 115 ACCATTCAAGTCCAGCCCTTGTTCAGGGGATCTCTGTGTGCTGACTCAACGACCCCGA 174
Db 213 GAATCGATGCCAACCAAAATTTCTTCAACAAATCCATAGTGAGACTCTCAGAACTGA 272
QY 175 TGCAAGAAATCTCATAGTGAACGCCCTGTAGGGACTTTCGGCTTCTTCAAGCTTGTGAACCA 234
Db 273 TGCAAGAGCCCTTATAGTGAAGCTTGTGAGGAGTTTGGATTCTTCAAGTCAATCA 332
QY 235 TGGTGTTCATTTGAGTTAATGCCAAATTTAGAAACGAGGCCCTCAGGTTCTTTAAAAA 294
Db 333 TGGTGTCTCATGGAAGCTATATCCGAATTTGGAATATGAAGCCCTTCAAAATTTCTCTAT 392
QY 295 ATCTCAGTCCGAGAAAGACAGAGCTGTCTCCCGCCCTTTTCGGCTATGTAGCAAGAG 354
Db 393 GTCACTCAATGAAGAAAGAAAGTAGAGCTCCCAATCCATTTGGGTATGTAGCAAGAA 452
QY 355 GATTGGCCCAACCGGTGATGTCGGTTGGGTGCGAATACCTCTCCTCAACACCAACCTGA 414
Db 453 AATTGGACACAATAGGAGCGTTGGTTGGATTGAGTACCTTCTTCTCAACCAATCAAGA 512

QY 415 TGTATATCACCACCAATCACTTTTGCATTTTCCGAGAAATCTCTCATCTTTCAGGSCGCT 474
Db 513 ACACAACT-----TCTCTGTTATGCGCAAAACCCCTGAGAAATTCAGGTGCT 560
QY 475 GGTGAGAACTACATTAACAGCAGTAGTGAAGAAATGTGCTATGCGGTGTTGGAAATTTGATGC 534
Db 561 GTTGAACAGTTACATGTCTTCTGTGAGGAAGATGCAATGTGAGATTCTTCTGAGTTGATGC 620
QY 535 GGAGGGTTGGGGATAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAG 594
Db 621 AGAAGGGTTGAAGATTTCAGCAAAAGGATGTGTTTAGCAAGCTTCTTAATGGATAAACAAG 680
QY 595 TGATTCGTGCTTCAGGTTGAACCACTACCGGCTTTCGCCCTGAGGTGCAAGCACTGAACCG 654
Db 681 TGACTCTATTTCAGGGTGAATCATTTACCTGCTGCTGCTGAAATGACTCTGAATGATCA 740
QY 655 GAATTTGGTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAA 714
Db 741 GAACTTGATTGGGTTTGGAGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCAA 800
QY 715 CAGCAGATCTGGCTTGCATAATCTGTCTCAGATGSCACTTGGGTTTCAGTCCCACTGA 774
Db 801 CAACACTTCAGGCCTTCAGATTATCTTAGAGATGGAAATTCGATTTCACTCCACCA 860
QY 775 TCAGACTTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAAATGGGAGGTT 834
Db 861 TGACAAATCCTTTTATTAACGTTGGTGATTTCTCTTCAGGTTATGACAAATGGAAGTT 920
QY 835 TAAAAGTGTAAAGCATAGGGTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTA 894
Db 921 CCGAAGTGTGACACACAGAGTGTTCGCAATGGGTTCAAGTCCAGGCTTTCATGATTTA 980
QY 895 CTTTGGAGGACAGCGTTGAGTGAAATATAGCACTTTACCTTCAGTCTGATGTTAAAGG 954
Db 981 CTTTGGAGGTCACCTTTTGAGTGAGAAAAATAGCACCATTATCCTCTCTCATG---AAAGG 1037
QY 955 AGAGGAGTGTGTTGACAAAGAGTTACATGTTGTGAATACAAAGAGGTCGCTACACTTC 1014
Db 1038 AAAAGAAAGTCTATATAAAGAGTTTACCTGGTTTGGATGACAAAATAATCAATCTACGGTTC 1097
QY 1015 AAGGCTAGCTGATAATAGGCTTTCGCCCTTTCCAGAAATCTGCTGTGATTAA 1066
Db 1098 AAGATTATCTAAAATAGACTTTGAACATTTTGAAGAAATTCGAGCTTCGTAA 1149

RESULT 5
US-09-719-108-7
; Sequence 7, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-719-108-7
Query Match 32.3%; Score 425.8; DB 3; Length 1237;


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Best Local Similarity 66.3%; Pred. No. 3.6e-116;
Matches 629; Conservative 0; Mismatches 317; Indels 3; Gaps 1;

QY 146 ATTCTGTGTGCGACTCAAGCAGCCGATGCAAGAAATCTCATAGTGAACCCCTGTAGG 205
Db 199 ATCCCGTGTCTCAACTAGCCGATCGGAGCGAAACCCGATCGTAAGCCCTCGAG 258
QY 206 GACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATTTGAGTTAATGCCCAATTGA 265
Db 259 GAGTTTCGGCTTCTCAAGCTGTGAACCATGGTGTTCATTTGAGTTAATGCCCAATTGA 318
QY 266 GAAACGAGGCGCTCAGGTTCTTTAAATAATCTCAGTCCGAGAAAGACAGAGCTGGTCC 325
Db 319 GAGCAGGAGGCTTAATGGCTTCTTCGGCTTTCAGCTCTCTCTCTCTCTCTCTCTCTCT 378
QY 326 CCGGACCCCTTCGGCTATGATGAGCAAGAGATTTGGCCAAACCGTGTGATGTTGGTGTG 385
Db 379 CTGGAACCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 438
QY 386 GAATACCTCTCTCAACACCAACCCCTGATGATGATGATGATGATGATGATGATGATGATG 445
Db 439 GAGTATCTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 498
QY 446 CGAGAAATCTCATCATTTTCAGGCGGTGTGGAGAACTACATTTACAGCAGTGAAGAC 505
Db 499 CGTCAACCCCTCAAAATTTTCGGTGTGATGATGATGATGATGATGATGATGATGATGAT 558
QY 506 ATGTGCTATGCGGTGTGGAATTTGATGCGGAGGAGTGGGATTAAGGCGAGAGGAATACG 565
Db 559 GTGTGCTACAGGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
QY 566 TTAAGCAGGTTTCTGAAGGATGAGAAAGTATGATGATGATGATGATGATGATGATGATG 625
Db 619 CTGAGTAAATCTCAGAGATGAGAGAGTACTCGTGCCTGAGACTAAACCATTTATCG 678
QY 626 CTTGCGCTGAGTGAAGCAGTGAACCGGAATTTGGTGGTGGTGGTGGTGGTGGTGGTGG 685
Db 679 GCG--GCGGAGGAGAGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 735
QY 686 CCACAGATAATTTCTGCTTAAGATCTAACACACATCTGGCTGCAATCTGCTCTACA 745
Db 736 CCACAGATAATCTCAGTGTAAAGATCTAATAACCGGCGTCTTCAATCTGCTGAA 795
QY 746 GATGCACTTTGGGTTTCAGTCCACCTGATCAGACTTCTTTTTCATCAATGTTGGTGAC 805
Db 796 GATGGAAGTTGGTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 855
QY 806 GCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGAAGCATAGGTTTGGCTGAC 865
Db 856 GCTCTTCAGGTTATGACTAACCGGAGGTTCAAGAGTGTATAACACAGGCTCTTAGCCGAT 915
QY 866 ACAACGAGTCAAGGTTATCAATGATCTACTTTGGAGGACAGGCTTGAGTGAATAATA 925
Db 916 ACAGAGATCAGAGATTTCAATGATATAATTTTCGGCGGACCCCATTTAGCCGAGATC 975
QY 926 GCACCTTTACCTTCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 985
Db 976 GCACCATTTGCCATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1035
QY 986 TGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCTGATATAAGGTTGCCCGCTTC 1045
Db 1036 TCTCAATAAATAATCTTCTGCTTACAGTCTAAGCTTGGTGTATATAGACTTGGTCTCTTT 1095
QY 1046 CAGAAATCTGCTGCTGATTAACCAACACACACCCCTTCAATTCACCTCAT 1094
Db 1096 GAGAAACAAACCTCTTCTCAATCATAAACCCCTTGTATGAGATGATGATCAT 1144

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RESULT 6

US-09-371-307-64
; Sequence 64, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:

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; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Pillier, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOST:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-371-307-64

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Query Match 32.2%; Score 424.8; DB 3; Length 1403;
Best Local Similarity 66.0%; Pred. No. 7.7e-116;
Matches 569; Conservative 0; Mismatches 327; Indels 18; Gaps 3;

QY 53 ACAACAAACAAACATGTTGTTCTGTCTCAGCCAGCATTTGAACAGTTTTCCTCTG 112
Db 134 AAAGCAGCAGAGAAATGTTGTTCTGTTCCAAGGCCAACACAGAACAAATCTCTACATC 193
QY 113 AACCAATTCAGTCCAGCCCTTGTTCACGGGGATTCCTGTGTCAGCTCAGCAGCCCC 172
Db 194 AAGAACTACATGCCAACCGCATTTCTCTCAACAAATTCCTGAGTGGAGCTCTCCAAACA 253
QY 173 GATGCAAGAAATCTCATAGTGAACCGCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAAC 232
Db 254 GATGCAAGACCCCTCATAGTGAAGCTTGTGAGGAAATTTGGATCTTCAAGTCTATCAAC 313
QY 233 CATGTTGTTCCATTTGAGTTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAA 292
Db 314 CATGTTGTTCCATGGAATATATATCCCAATTTGGAATCTGAAAGCCCTTCAAGTCTTCTCT 373
QY 293 AAATCTCAGTCCGAGAAACAGAGCTGTTCCCCCGACCTTTCGGCTATGTTAGTACAG 352
Db 374 ATGCCACTCAATGAGAGGAAAGATAGGCCCTCCCAACCATATGTTGGTATGTTAGCAG 433
QY 353 AGGATTTGCCCAACCGGTGATGTCGGTTGGGTGCGAATACCTCTCTCAACACCAACCTCT 412
Db 434 AAATTTGACACAAATGGGATGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTT 493
QY 413 GATGTTATCTCAACCAATCACTTTTGCAATTTTCCGAGAAAATTCCTCATCATTTTCAGGG 472
Db 494 GAACACAACT-----TCTCTGTTTATGGCAAAAACGCTGAGAAAATTTAGGTGT 541
QY 473 GTGGTGGAGAACTACATTTACAGCAGTGAAGACATGCTATGCGGTGTGGAATTTGATG 532
Db 542 TTGTTGAACAGTTACATGCTCTTCTGTGAGGAAAATGGCATGTGAGATTTCTTGAGCTGATG 601
QY 533 GCGGAGGGGTTGGGATTAAGCAGAGGAATACGTTTAAGCAGAGTTGCTGAAGGATGAGAAA 592
Db 602 GCAGAGAGATTTGAAGATACAAACAAAATGTTTATGAGAGCTTCTTATGATTAAGAG 661
QY 593 AGTGAATTCGTCTCAGGTTGAACCACTACCGGCTTCCCTCCTGAGGTGCAAGCACTGAAC 652
Db 662 AGTGAATCTGTTTTTATGGGTGAATCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
QY 653 CGGAATTTGTTGGTTTGGGGAGCAGACAGACCCACAGATAATTTCTGTCTTAAGATCT 712
Db 719 CAAACATGATAGGTTTGGAGAACACACGACCCCAAAATCAATTTCTCTACTTAGGTCC 778
QY 713 AACGACATCTGCTTCAAAATCTGTCTCAGATGGCAGCTTGGGTTTTCAGTCCACCT 772
Db 779 AACAACTTTCAGGCTTCAGATTTTCTTAGAGATGGAATCTGGAATTTTCAGTCCACCT 838

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		PRIOR FILING DATE: 1999-12-21 NUMBER OF SEQ ID NOS: 204 SOFTWARE: Microsoft Office 97 SEQ ID NO 7 LENGTH: 1473 TYPE: DNA ORGANISM: Triticum aestivum US-09-614-912-7		Query Match Best Local Similarity 27.6%; Score 363.6; DB 3; Length 1473; Matches 607; Conservative 0; Mismatches 374; Indels 9; Gaps 1;	
QY	60	CAACACCAATGGTGTGTTCTCTCAGCCAGCATTTGAACCAAGTTTTCCTTCTTGAACCAAT	119		
DB	119	CAGCCATGGTGTCTCGCCAGCAGCCCGCGTGCATCAGTCCGCTCTCAGTCCG	178		
QY	120	TCAAGTCCAGCCCTTGTTCAGGGGATTCCTGTGGTGCACCTCAGCACCCCGCATGCCA	179		
DB	179	CGACCCCGGGGACTACTTCTCGGCATCGCGTGTGTCACCTCTCCAGCCCTGGCGGC	238		
QY	180	AGAACTCATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGT	239		
DB	239	CGGGGCCATCGCGACGCTGGAGCGCTTCGGGTCTTCAAGCTTCGTCACACCGGG	298		
QY	240	TTCCATTGAGTTAATGGCCAAATTTAGAAAAAGAGCCCTCAGGTTCTTTAAAAAATCTC	299		
DB	299	TGCCCCGCGACGATGGACAGCTCGAGTCGGAGGCCGTCAAGTTCTTCTCGCTGCCG	358		
QY	300	AGTCCGAGAAAGACAGAGCTGTGCCCCCGACCTTTCGGCTATGTTAGCAGAGATTG	359		
DB	359	AGCGCCACAAAGACCCCTCCGCGCCCGCTACCCGTTCCGCTACGGCAGCAAGCGCATG	418		
QY	360	GCCAAACGCTGATGTCGGTGGTGCATACCTCTCTCAACACCAACCCCTGATGTTA	419		
DB	419	GGTCAATGGACATGGGGTGCTCGAGTACTCTCTCGCGTGCAGTCCGCTCGCTCGC	478		
QY	420	TCTCAACCAATCACTTTGTCATTTTCCGAGAAAAATCCTCATCATTTTCAGGCGGTGGTGG	479		
DB	479	TCTCCGCGCTCGCGCGTCCGCTCTCGC-----CGCTCTTCGGCGCGCTGA	529		
QY	480	AGAACTACATTCAGCAGTGAAGAACATGTGCTATCGCGTGTGGAATGATGGCGGAG	539		
DB	530	ACGAGTACATCGCGCGTTCGGAAGTGGCGGTGATGAGGCGATGGCGGAGG	589		
QY	540	GGTTGGGATAGGCAGAGATACGTTAAGCAGGTTCTGAGGATGAGAAAGTATT	599		
DB	590	GGCTGGGCATTCGCGCGTGGACGCGCTGAGCGGGATGGTGCAGCGGGAGGGAGCGACC	649		
QY	600	CGTGTCTCAGGTTGAACCACTACCCCGCTTGCCCTGAGGTGCAAGCACTGAACCGGAATT	659		
DB	650	AGGTGTTCCGGGTGAACCACTACCCCGCTGCCACGCGCTGCAGGGCTGGGTGCAGGG	709		
QY	660	TGGTTGGGTTTGGGAGACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCA	719		
DB	710	CCACCGGCTTCGCGAGACACAGGACCCGCGCTCATCTCCGCTGCTGCCTCAACGGCA	769		
QY	720	CATCTGGCTTGAATCTGCTCAGAGATGGCACTTGGGTTTCAGTCCACCTGATCAGA	779		
DB	770	CGTCCGCGCTGCAGATTCGCGCTCCAGAACGGGCGTGGGTGTCGTCCTCGACCCGG	829		
QY	780	CTTCTCTTTTCATCAATGTGTGTGAGCTCTACAGGTAAATGACTAATGGGAGGTTTAAAA	839		
DB	830	ACGCTTCTTCGTCACAGTCCGGGACTCGTTGACGCTGCTGACCAACGGGAGGTTCAAG	889		
QY	840	GTGTAAAGCATAGGGTTTGGGTGACACAAACGAAGTCAAGGTTATCAATGATCTACTTGG	899		
DB	890	GGGTGAAGCACAGGGTGGTGGCCAAACAGCCCTAAAGTCTAGGGTTTCCATGATCTACTTGG	949		
QY	900	GAGGACCGGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGTGTTTAAAGGAGAGG	959		
DB	950	GAGGGCCAGCGATGACACAGAGGATTTGCACCAATTCGCCGAGCTGTGGCGCGGGAGAGC	1009		

		RESULT 9 US-09-719-108-5 Sequence 5, Application US/09719108 Patent No. 6670527 GENERAL INFORMATION: APPLICANT: Thomas, Stephen G APPLICANT: Hedden, Peter APPLICANT: Phillips, Andrew L TITLE OF INVENTION: Gibberellin 2-Oxidase FILE REFERENCE: 0623.0970000 CURRENT APPLICATION NUMBER: US/09/719,108 CURRENT FILING DATE: 2000-12-08 PRIOR APPLICATION NUMBER: PCT/GB99/01857 PRIOR FILING DATE: 1999-06-11 PRIOR APPLICATION NUMBER: GB 9812821.8 PRIOR FILING DATE: 1998-06-12 PRIOR APPLICATION NUMBER: GB 9815404.0 PRIOR FILING DATE: 1998-07-15 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 5 LENGTH: 1318 TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE: NAME/KEY: misc feature LOCATION: (1243, 1265) OTHER INFORMATION: unidentified residue US-09-719-108-5		Query Match Best Local Similarity 27.1%; Score 356.6; DB 3; Length 1318; Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;	
QY	132	CTTCTTTCACGGGATTCCTGTGTGCGACCTCACACCCCGATGCCAAGATCTCATAG	191		
DB	78	CGGGTCTCTCTAATCCGGTTATAGATATGCTGACCCAGAAATCCAAACATGCCCTCG	137		
QY	192	TGAACGCTGTAGGACCTTCGCTTCTTCAAGCTTGTGNAACCATGGTGTTCATTTGAGT	251		
DB	138	TGAAGCATGCGAAGACTTCGGCTTCTTCAAGGTGATCAACCATGGCGTTTCCGACAGAG	197		
QY	252	TAAATGCCCAATTTAGAAAAAGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAG	311		
DB	198	TAGTCTCTGTTTTAGAACACAGACCGTGCATTTCTTCTGTTGCCAAGTCAGAGAA	257		
QY	312	ACAGAGCTGGTCCCGCCGACCCCTTTCGGCTATGTTAGCAAGAGGATGTCGCCAACCGTG	371		
DB	258	CCCAAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAAGATTGTCGGAATGGTG	314		
QY	372	ATGTCGGTTGGGTGGAATACCTCTCTCCCAACCAACCCCTGATGTTATCTCACCCAAAT	431		
DB	315	ACGTGGTGGGTGAGTACTTGTGTGAGAACCGCTAATCATGATTCGGGTTCGGGTCCAC	374		
QY	432	CACTTTGCAATTTTCGAGAAAAATCTCATCTTTCAGGCGGTGGTGGAGAACTACATTA	491		
DB	375	TATTTCCAGTCTTCTCAAAAGCCCGGAACTTTTCAGAAACCATTTGGAAGAGTACACA	434		
QY	492	CAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTTGATGGCGAGGGTGGGGATAA	551		
DB	435	CATCAGTGAGAAAAATGACATTCGATGTTTTGAGAGAGATCACAGATGGGTAGGATCA	494		
QY	552	GGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAAGTGTTCGTGCTTCAGGT	611		

Db 495 AACCGAGGAAACACACTTTAGCAAGCTTGTGTCTGACCAAAACACGAGCTCGATATTGAGAC 554
QY 612 TGAACCACTACCCGCTTGGCCCTGAGGTGCAAGCACTGAAAC-----CGGAATTTGG 662
Db 555 TTAATCATACTCCACCAATGCTCTTTAGCAATAGAAACCAATGGTGTAAAGATGTGA 614
QY 663 TTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAAGATCTTAAACAGCACAT 722
Db 615 TTGGTTTGGTGAACACACAGATCCTCAATCATCTCTGTCTTAAAGATCTTAAACACACTT 674
QY 723 CTGGCTTGCAAACTGTCTCACAGATGGCACTTTGGGTTTCAAGTCCCACTGATCAGACTT 782
Db 675 CTGGTCTCCTCAAAATTAATCTAAATGATGGCTCATGGATCTCTGTCCCTCCCGATCACACTT 734
QY 783 CTTTTTTTCATCAATGTTGGTGACGCTCTACAGGTAAATGACTAATGGAGGTTTAAAGTG 842
Db 735 CCTTCTTCAACGTTTGGTGACTCTCTCAGGTGATGACAAATGGAGGTTTCAAGAGCG 794
QY 843 TAAAGCATAGGTTTGGCTGACACAAACGAAGTCAAGGTTTATCAATGATCTACTTTGGAG 902
Db 795 TGAGGCATAGGTTTGTAGCTAACTGTAAAAAATCTAGGGTTTCTATGATTTACTTTCGCTG 854
QY 903 GACACGTTGAGTGAATAATAGACACTTTTACCTTCAGTGATGTTAAAGAGAGAGAGT 962
Db 855 GACCTTCAATGACTCAGAGAAATCGCTCCGTTGACATGTTTGTATAGACAATGAGGACGAGA 914
QY 963 GTTTGTACAAAGAGTTTACATGTTGTGAATACAAAGAGGCTGCTACACTTCAAGGCTAG 1022
Db 915 GGTGTACAGGAGTTTACTTGTGCTGAATACAAAAAATCTACTACAACTCTAGATTGT 974
QY 1023 CTGATAATAGGCTTGCCCTTTCCAGA 1049
Db 975 CTGATAATAGGCTTCAACRAATTCGAAA 1001

RESULT 10
US-09-614-912-3
; Sequence 3, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafaleski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Ramodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-614-912-3

Query Match 26.9%; Score 354; DB 3; Length 1650;
Best Local Similarity 60.9%; Pred. No. 1e-94;
Matches 598; Conservative 0; Mismatches 375; Indels 9; Gaps 1;
QY 69 TGGTGTCTGTCTCAGCCAGCAATTTGAACACAGTCTTTTCTCTCTGAAACCAATTTCAAGTCCA 128
Db 132 TGGTCTCGCTGGCCGCGCGCTCGATCACATCCCGCTGCTGAGGTGCGCGGACCCCG 191
QY 129 CGCCCTTGTTCAGGGGATTTCTGTGTGTCGACTCAGGCACCCCGATGCAAGAATCTCA 188
Db 192 GCGACGCTTCTCCGCGCTGCGGCTGTCGACCTCGGCAGCCCGCGCGGAGGCGCG 251
QY 189 TAGTGAACCCCTGTAGGGATTTCTGCGCTTCTTCAAGCTTGTGAACCAATGTTTCCATTGG 248
Db 252 TGGTGAACCCCTGCGAGCGGTACGGGTTCTTCAAGTCTGCAACACGCGGTGGCCACGG 311
QY 249 AGTTAATGCCCCTAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGA 308
Db 312 ACACGATGACAAAGGCGAGTGGAGGCGCTCAGGTTCTTCTCCAGACGCGAGCCCGACA 371
QY 309 AAGACAGAGCTGGTCCCGCGACCTTTTCGGCTATGTTAGCAAGAGATTTGGCCCAACG 368
Db 372 AGGACCGCTCCGCGCCCGGCTTACCCGTTTCGGGTACGCGCAGCAAGCGGATCGGGTTCAATG 431
QY 369 GTGATGTCGGTTGGGTGCAATACCTCTCTCAAACCAACCAACCTGATGTTATCTCACCCA 428
Db 432 GCGACATGGGTGGCTGAGTACCTCTCTCGCCCTCGACGCGCTGCTCGCCGACG 491
QY 429 AATCACTTTGCAATTTTCCGAGAAAAATCTCATCATTTTCAGGGCGGTGGTGGAGAACTACA 488
Db 492 CTTGACACCGTCCGCTCTCG-----CGGTCTTCCGGGCGCTCTGAACGAGTACA 542
QY 489 TTACAGCACTGAAGAACATGTGCTATGCGGTGTTGGAATTTGATGCGCGAGGGTTGGGGA 548
Db 543 TCTCGGGGTGCGGAAGTGGCGGTGATGGAAGCGATGTGCGAGGGGCTGGGCA 602
QY 549 TAAGGCAGAGGAATACGTTAAGCAGGTTCTGTAAGGATGAGAAAGTGAATCGTGTCTCA 608
Db 603 TTGCGCAGCGGACGCGCTGAGCGCTGTGTAACGCGGAAGGAGCGACAGGTGTTCC 662
QY 609 GGTGAACCACTACCCGCTTGCCTTGAGGTGCAAGCACTGAAACCGGAATTTGGTTGGGT 668
Db 663 GCGTGAACCACTACCCGCGCTGCGCGCTGCGAGGGCTCGGCTGCAGCGTCAACGGCT 722
QY 669 TTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAAGACACATCTGGCT 728
Db 723 TCGGCGAGCACACCGACCCGCGAGCTGCTCTCGCTCCGCTCAACCGGACGTCGCGGC 782
QY 729 TGCMAATCTGTCTCACAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCTCTTT 788
Db 783 TGCAGATCGGCTCCGCGACGCGCAGTGGGTGTCGCTGCGCTCCGACCGGACTCTCTTCT 842
QY 789 TCATCAATGTTGGTGAACGCTCTACAGGTAAATGACTAATCGGAGGTTTAAAGTGTAAAGC 848
Db 843 TCGTCAACGTCGCGCACTCGTTGCAAGTTCTGACCAATGGAGGTTTCAAGAGCGTGAAGC 902
QY 849 ATAGGTTTGGCTGACACACAGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAG 908
Db 903 ACAGGGTGGTGGCCCAACAGCCTTAAAGTCTAGGGTTTCTTCTACTTTGGAGGGCCAC 962
QY 909 CGTTGAGTGAAATATAGCACCTTTTACCTTTCAGTGTATGTTTAAAGGAGGAGGTGTTGT 968
Db 963 CGTTAGCACAGAGGATTTGACCAATTTGCCACAGCTGCTGGGGGAGGAGCAGAGCTGT 1022
QY 969 ACAAGAGTTCAATGGTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGATA 1028
Db 1023 ACAAGGAGTTCAATGGGATGAGTACAAAGAGGCTGCTTACAAATCAAGGCTTGGAGACA 1082
QY 1029 ATAGGCTTGGCCCTTTCAGAA 1050
Db 1083 ACAGGCTGGCCCGAGTTTGAGAA 1104


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RESULT 11
US-09-614-912-1
; Sequence 1, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Cai, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: B01378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1555
; TYPE: DNA
; ORGANISM: Zea mays
US-09-614-912-1

Query Match      24.0%; Score 315.8; DB 3; Length 1555;
Best Local Similarity 58.9%; Pred. No. 2.4e-83;
Matches 586; Conservative 0; Mismatches 397; Indels 12; Gaps 2;

QY 59 ACAACACCATGGTGTCTGTCTCAGCCAGCAATGAACACGATTTTCTCTCTGAAACCA 118
DB 112 ACAGCCATGGTGTCTGCCAAACCGCTGTCTGCACCAATCCCGTCTCTGGGTCC 171
QY 119 TTCAAGTCCACGCCCTTTTTCACGGGATTCCTGTGGTGCACCTCACGCCACCCCGATGCC 178
DB 172 CCGGGCCCCCAGGACAGCTTCTCGGAGTGCCTGTCTGACCTGTCCAGCCACCGCGCG 231
QY 179 AGAATCTCATAGTGAACGCTGTAGGACTTTCGGCTTCTCAAGCTTGTGAACCATGGT 238
DB 232 CGCGGGCGCATCGTCAAGCCCTCGAGCGCTTCGGGTCTTCAAGTCTCGTCAACCAACCGC 291
QY 239 GTTTCATTTCGAGTGAATGCCCAATTTAGAAAACGAGGCCCTCAGGTCTCTTTAAAAAATCT 298
DB 292 GTGGCGGGCCACCATGACAGGGCCGAGTCCGAGGCCGTCAAGTCTTCGCGCAGGGG 351
QY 299 CAGTCCGGAAGACAGAGCTGGTCCCCCGACCCCTTTTCGGCTATGGTAGCAAGAGGATT 358
DB 352 CAGGCGGACAGGACCGCGCGCGCGGTACCCGTTCCGGTACGGCAGCAAGCGGATC 411
QY 359 GGCCCAACCGGTGATGTGGTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTT 418
DB 412 GGGCTCAATGGCGACATGGGGTGGTTCGAGTACCTCTCTCGCGTGCACGCCGCTCG 471
QY 419 ATCTCACCCCAATCACTTTGCAATTTCCGAGAAATCCTCATCATTTTCAGGCGGTGGT 478
DB 472 CTCTCCGAGCGCTGCCCGGTGCCCTCCAGCG-----CGCGTTCGGAGCGCGTGT 522
QY 479 GAGAACTACATTACAGCAGTGAAGAACATGTCTATGCGGTGTGGAATTGATGGCGGAG 538

523 AACGAGTACGTGCGCGCGTGCAGGAAGGTGGCGCGCGTGTGCTGGAGCGATGGCGGAG 582
539 GGGTTGGGGATAAGGCAGAGGAATAAGTTAAGCAGGTTGCTCAAGGATGAGAAAAAGTGTAT 598
583 GGCCTGGGCATTTGGGACCGGACCGGCTGAGCTTCATGGTAGCGGCCCGCGGAGCGAC 642
599 TGTGCTTTTTCAGGTTGAACCACTACCCGCTTTGCCCTGTAGGTTGCAAGCACTGAACCGGAAT 658
643 CAGGTGTTTCGCGTGAACCACTACCCGCTTCCGCGCGCTGCGAGGGCTGGGCTGCAGC 702
659 TTGTTGGGTTTGGGAGCAGACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGC 718
703 ACCACGGGCTTTGGCGAGCAGACACCGACCCGAGATCATCTCCGTCTCGCTCCAAACGCG 762
719 ACATCTGGCTTGCAAAATCTGTCTACAGATGGCAC---TTGGGTTTTCAGTCCCACCTGAT 775
763 ACCTCGGCTGAGATCGCGCTCGCGACGGCGGAGTGGGTCTCGGTGCCCTCCGAC 822
776 CAGACTTCTTTTTCATCAATGTTGGTGCAGCTCTACAGGTAAATGACTAAATGGGAGGTTT 835
823 CGCGACGCTTCTTCTGTTAAAGTTCGGGCTCGTTCAGGTCGTGACCAACCGGAGGTTT 882
836 AAAAGTGTAAAGCATAGGTTTGGCTGACACCAAGCAAGTCAAGTTATCAATGATCTAC 895
883 AGGAGCGTGAAGCACCGGGTGTGACCAACAGCTTCAAGTCCAGAGTTTCTTTCATCTAC 942
896 TTTGGAGGACCGGCTTCAGTGAAATATAGCACCTTTTACCTTTCAGTGTATTTAAAGGA 955
943 TTGCGGGGCGCGCTCGGCGAGGGATTCGCGCGCTGCGCGAGTGTGCGCGAGGGA 1002
956 GAGGAGTGTGTTGTAACAAAGAGTTTCAATGGTGTGTAATACAAAGAGCGCTGCTACACTTCA 1015
1003 GAGGAGAGCTGTACAGAGGTTTACAGTGGGCGAGTACAGAGGCGCGGTACAGAGCG 1062
1016 AGGCTAGCTGATATAGGCTTGGCCCTTTTCAGAA 1050
1063 AGGCTCGCGACACACAGGCTGGCCCGAGTTTGAGAA 1097

RESULT 12
US-09-371-307-67
; Sequence 67, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Filler, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOST:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 67
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (726)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-67

Query Match      23.6%; Score 311; DB 3; Length 783;
Best Local Similarity 70.1%; Pred. No. 4.4e-82;
Matches 441; Conservative 0; Mismatches 170; Indels 18; Gaps 1;
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Query Match 11.8%; Score 155.6; DB 3; Length 403;
Best Local Similarity 63.2%; Pred. No. 5.8e-36;
Matches 261; Conservative 0; Mismatches 140; Indels 12; Gaps 1;

QY 284 TTCCTTAAATAATCTCAGTCGCGAGAAACACAGAGCTGGTCCCGACGCTTCCGGCTAT 343
DB 2 TTCCTTCTCTATGTCACTCAATGAAAGAAAGATAGGACCTCCCAATCCATTTGGGTAT 61

QY 344 GGTAGCAAGAGATTGGCCCAACCGGTGATGTCGGTTGGGTGCGAATAGCTCTCTCAAC 403
DB 62 GGTAGCAAGAAATTTGGACACATGGGACGTTGGTTGGATTGAGTACCTTCTTCTCAAC 121

QY 404 ACCAACCTGTATGTTATCTCAACCAATCCTTTGCATTTTCCGAGAAATCCTCATCAT 463
DB 122 ACCAATCAAGAACCACT-----TCTCTGTTTATGGCAAAACCCCTGAGAAA 169

QY 464 TTCAGGCGGTGGTGGAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTG 523
DB 170 TTCAGGTGCTGTTGAACAGTTTACATGCTTCTGTGAGGAAAGATGGCATGTGAGATTCTT 229

QY 524 GAATTTGATGGCGAGGGTGGGATAAGGCGAGAGGAATACGTTAAGCAGGTTGCTGAAG 583
DB 230 GAGTTGATGGCAGAGGGTTGAAGATTCAGCAAGAGGATGTTTAGCAGCTTCTAATG 289

QY 584 GATGAGAAAGTGATTCGTGTTCAAGTTGAACCACTACCCGCTTGCCTGAGGTGCAA 643
DB 290 GATAAACAAAGTGACTCTATTTTTTCAGGCTGAATCATTACGCTGCTTGTCTGAAATGACT 349

QY 644 GCAGTGAACCGGAATTTGGTGGTTTGGGAGCAGACAGACCCACAGATAAT 696
DB 350 CTGAATGATCAGAACTTGAATTTGGGTTTGGAGAACACAGACCCCAAAATCAT 402

RESULT 15

US-09-371-307-68
; Sequence 68, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Filler, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 68
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (306)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-68

Query Match 11.7%; Score 154.8; DB 3; Length 406;
Best Local Similarity 66.6%; Pred. No. 1e-35;
Matches 279; Conservative 0; Mismatches 113; Indels 27; Gaps 3;

QY 314 AGAGCTGTGTCCTCCCGACCTTTCGGCTATGCTAGCAGAGGATGGCCCAACCGTGAT 373
DB 2 AAACAGGACACACCCCGCTTATGGCTATGCTATGATTAAGGATTTGGACCAATGGTGAT 61

QY 374 GTCGGTTGGGTGGAATACCTCTCTCAACCAACCCCTGATGTTATCTCACCCAAATCA 433

DB 62 GTTGGTTGGGTGGAATATCTTCTCTCACAACCAACCAAG-----ACCCGAATCT 111
QY 434 CTTTGCATTTTCCGAGAAATCCTCATCATTTTCCAGGCGGTGGTGGAGAACTACATTACA 493
DB 112 CTTTGGAACT-----GAAACCCAGAGAGTTTTCAGGATTGCTTTGGATAATTATATGCA 166

QY 494 GCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTTGATGGCGGAGGGTTGGGGATAAGG 553
DB 167 GCAGTGAAGAAATGGCATGTGAGATACCTTGAATGATAGCTGATGGGCTAAAGGTTTCA 226

QY 554 CAGAGGAATACGTTAAGCAGGTTGCTGNAAGATGAGAAAGTGAATTCGTGCTTCAGGTTG 613
DB 227 CCAGAAATGTGTTAAGTAAAGCTGATGATGGATGAACACAGAGTGACTCTGTTTTCAGGCTG 286

QY 614 AACCACTACCCGCTTGCCTTGAGG-----TGCAAGCACTCAACCCGGAATTTG 661
DB 287 AACCATTACCTCCGTGCCNAGAGGTGGTTCAAGTCCCTTGAATGGNACGAGCAGTAATGTG 346

QY 662 GTTGGGTTTGGGAGACACACAGACCCACAGATAATTTCTGTTCTTAAGATCTAAACAGCAC 720
DB 347 ATTGGATTGCGTGAACACACACTGACCCCAAAATCATTTCAGTCTTAAGATCCCAACACAC 405

Search completed: December 28, 2005, 00:46:40
Job time : 272.271 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1318	100.0	1318	8	US-10-670-454-1	Sequence 1, Appli
2	999	75.8	999	8	US-10-821-711-3	Sequence 3, Appli
3	893.8	67.8	1359	3	US-09-371-307-62	Sequence 62, Appl
4	893.8	67.8	1359	6	US-10-401-321-62	Sequence 62, Appl
5	425.8	32.3	1237	8	US-10-670-454-7	Sequence 7, Appli
6	425.4	32.3	1026	3	US-09-938-842A-1350	Sequence 1350, Ap
7	425.4	32.3	1026	3	US-09-938-842A-1350	Sequence 1350, Ap
8	424.8	32.2	1403	3	US-09-371-307-64	Sequence 64, Appl
9	424.8	32.2	1403	6	US-10-401-321-64	Sequence 64, Appl
10	397.6	30.2	1390	7	US-10-424-599-21951	Sequence 21951, A
11	382.8	29.0	1008	8	US-10-670-454-9	Sequence 9, Appli
12	356.6	27.1	1318	8	US-10-670-454-5	Sequence 5, Appli
13	354	26.9	984	7	US-10-392-325-3	Sequence 3, Appli
14	354	26.9	1260	7	US-10-437-963-78659	Sequence 78659, A
15	315.8	24.0	1611	8	US-10-425-115-69575	Sequence 69575, A
16	311	23.6	783	3	US-09-371-307-67	Sequence 67, Appl
17	311	23.6	783	6	US-10-401-321-67	Sequence 67, Appl
18	302.8	23.0	831	7	US-10-425-114-6183	Sequence 6183, Ap
19	285	21.6	997	6	US-10-259-194A-141	Sequence 141, App
20	279.2	21.2	591	7	US-10-424-599-99278	Sequence 9278, Ap
21	273.8	20.8	860	7	US-10-424-599-129307	Sequence 129307, A
22	273.8	20.8	860	7	US-10-425-114-7861	Sequence 7861, Ap
23	203.2	15.4	1008	7	US-10-437-963-16086	Sequence 16086, A


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181 GAATCTCATAGTGAACGCTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACCAATGGTGT 240
241 TCATTTGGAGTTAATGSCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA 300
241 TCATTTGGAGTTAATGSCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA 300
301 GTCCGAGAAAGACAGAGCTGGTCCCCCGACCCCTTTCCGGCTATGGTAGCAAGAGATTGG 360
301 GTCCGAGAAAGACAGAGCTGGTCCCCCGACCCCTTTCCGGCTATGGTAGCAAGAGATTGG 360
361 CCCAAACGGTGATGTCGGTTGGTGGTGAATACCTCTCTCAACACCAACCCCTGATGTTAT 420
361 CCCAAACGGTGATGTCGGTTGGTGGTGAATACCTCTCTCAACACCAACCCCTGATGTTAT 420
421 CTCACCCAAATCACTTTGCAATTTCCGAGAAATCTCATATTTCCAGGCGCGTGTGGA 480
421 CTCACCCAAATCACTTTGCAATTTCCGAGAAATCTCATATTTCCAGGCGCGTGTGGA 480
481 GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATTTGATGCGGAGGG 540
481 GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATTTGATGCGGAGGG 540
541 GTTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC 600
541 GTTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC 600
601 GTGCTTCAGGTTGAACCACTACCGGCTTGCCCTGAGGTGCAAGCACTGAACCGGAATTT 660
601 GTGCTTCAGGTTGAACCACTACCGGCTTGCCCTGAGGTGCAAGCACTGAACCGGAATTT 660
661 GGTGGGTTTGGGAGCACACAGCCACAGATAATTTCTGTCTTAAGATCTAAACAGCAC 720
661 GGTGGGTTTGGGAGCACACAGCCACAGATAATTTCTGTCTTAAGATCTAAACAGCAC 720
721 ATCTGCTTCGAAATCTGTCTCAGATGCGACTTGGGTTTCACTCCACCTGATCAGAC 780
721 ATCTGCTTCGAAATCTGTCTCAGATGCGACTTGGGTTTCACTCCACCTGATCAGAC 780
781 TTCCTTTTTCATCAATGTTGGTGACCTCTACAGGTAATGACTTAATGGGAGGTTTAAAG 840
781 TTCCTTTTTCATCAATGTTGGTGACCTCTACAGGTAATGACTTAATGGGAGGTTTAAAG 840
841 TGTAAAGCATAGGTTTGGCTGACACACAGAGTCAAGGTTATCAATGATCTACTTTGG 900
841 TGTAAAGCATAGGTTTGGCTGACACACAGAGTCAAGGTTATCAATGATCTACTTTGG 900
901 AGGACAGCGTTGAGTGAAAATATAGCACTTTACCTTCAGTGATGTTTAAAGGAGGAG 960
901 AGGACAGCGTTGAGTGAAAATATAGCACTTTACCTTCAGTGATGTTTAAAGGAGGAG 960
961 GTGTTTGTACAAAGGTTACATGTTGTAATCAAGAGGCTGCGTACACTTCAAGGCT 1020
961 GTGTTTGTACAAAGGTTACATGTTGTAATCAAGAGGCTGCGTACACTTCAAGGCT 1020
1021 AGCTGATAATAGGCTTGCCTTTCCAGAAATCTGCTGCTGATTAACCAACACACCCCTT 1080
1021 AGCTGATAATAGGCTTGCCTTTCCAGAAATCTGCTGCTGATTAACCAACACACCCCTT 1080
1081 CAAATTCACATATTTTACGCGATTAATACCCCAATTTCTTCTTTTCTTTTCTTCC 1140
1081 CAAATTCACATATTTTACGCGATTAATTAACCCCAATTTCTTCTTTTCTTTTCTTCC 1140
1141 TGTGTCGTCTAGGTTTCAACAGTTGACTCTACTTGTGACATATATAGAAAATGAATAGGT 1200
1141 TGTGTCGTCTAGGTTTCAACAGTTGACTCTACTTGTGACATATATAGAAAATGAATAGGT 1200
1201 TAAGATGTTTATCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTT 1260
1201 TAAGATGTTTATCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTT 1260
1261 CCCTTTCCTCAATGTGCAATGGAACGCACTTAGTTTACAAAATAAAAAA 1318
1261 CCCTTTCCTCAATGTGCAATGGAACGCACTTAGTTTACAAAATAAAAAA 1318

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RESULT 2
US-10-821-711-3
; Sequence 3, Application US/10821711
; Publication NO. US20040237142A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieser, Blysia K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Wanggen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; FILE REFERENCE: 38-21(52967)B
; CURRENT APPLICATION NUMBER: US/10/821,711
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-10-821-711-3

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```

Query Match 75.8%; Score 999; DB 8; Length 999;
Best Local Similarity 100.0%; Pred. No. 2.1e-281; Indels 0; Gaps 0;
Matches 999; Conservative 0; Mismatches 0;

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QY 68 ATGGTTGTTCTCTCAGCAGCATGAAACCAAGTTTTCCTTCTGAAACCAATTCAGATCC 127
DB 1 ATGGTTGTTCTCTCAGCAGCATGAAACCAAGTTTTCCTTCTGAAACCAATTCAGATCC 60
QY 128 AGCCCTTGTTCACCGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAGATCTC 187
DB 61 AGCCCTTGTTCACCGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAGATCTC 120
QY 188 ATAGTGAACGCGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCCATTC 247
DB 121 ATAGTGAACGCGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCCATTC 180
QY 248 GAGTTAAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
DB 181 GAGTTAAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
QY 308 AAAGCAGAGCTGTGTCCTCCCGACCTTTTCGGCTATGGTAGCAAGAGGATTCGCCCAAC 367
DB 241 AAAGCAGAGCTGTGTCCTCCCGACCTTTTCGGCTATGGTAGCAAGAGGATTCGCCCAAC 300
QY 368 GGTGATGTCGGTTGGTTCGAATACCTCTCTCAACCAACCCCTGATGTTATCTCACCC 427
DB 301 GGTGATGTCGGTTGGTTCGAATACCTCTCTCAACCAACCCCTGATGTTATCTCACCC 360
QY 428 AAATCACTTTGCAATTTCCGAGAAATCTCATCATTTTCAGGCGGTGTGGAGAACTAC 487
DB 361 AAATCACTTTGCAATTTCCGAGAAATCTCATCATTTTCAGGCGGTGTGGAGAACTAC 420
QY 488 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAAATTCATGCGGAGGGGTTGGGG 547
DB 421 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAAATTCATGCGGAGGGGTTGGGG 480
QY 548 ATAAGGCGAGGAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTCTTC 607
DB 481 ATAAGGCGAGGAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTCTTC 540
QY 608 AGGTTGAACCACTACCCGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGG 667
DB 541 AGGTTGAACCACTACCCGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGG 600
QY 668 TTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGCC 727
DB 601 TTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGCC 660

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QY 728 TTGCAAAATCTGTCTACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTT 787
 DB 661 TTGCAAAATCTGTCTACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTT 720
 QY 788 TTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTTAATGGGAGGTTTAAAGTCTAAG 847
 DB 721 TTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTTAATGGGAGGTTTAAAGTCTAAG 780
 QY 848 CATAGGGTTTGGCTGACACAACGAAGTCAAGGTTTATCAATGATCTACTTTTGGAGGACCA 907
 DB 781 CATAGGGTTTGGCTGACACAACGAAGTCAAGGTTTATCAATGATCTACTTTGGAGGACCA 840
 QY 908 GCGTTGAGTGAATAATATAGCACTTTACCTTCAGTGAATGTTTAAAGGAGAGGAGTGTG 967
 DB 841 GCGTTGAGTGAATAATATAGCACTTTACCTTCAGTGAATGTTTAAAGGAGAGGAGTGTG 900
 QY 968 TACAAGAGTTCACATGGTGTAATACAGAGAGGCTGCTACACTTCAAGGCTAGCTGAT 1027
 DB 901 TACAAGAGTTCACATGGTGTAATACAGAGAGGCTGCTACACTTCAAGGCTAGCTGAT 960
 QY 1028 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGATTA 1066
 DB 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGATTA 999

RESULT 3

US-09-371-307-62
 ; Sequence 62, Application US/09371307A
 ; Patent No. US20020053095A1
 ; GENERAL INFORMATION:

; APPLICANT: Brown, Sherri M.
 ; APPLICANT: Heck, Gregory R.
 ; APPLICANT: Pillier, Kenneth J.
 ; APPLICANT: Kishore, Ganesh M.
 ; APPLICANT: Ellich, Tedd D.
 ; APPLICANT: Logusch, Eugene W.
 ; APPLICANT: Rao, Sudabathula
 ; APPLICANT: Ream, Joel E.
 ; APPLICANT: Logusch, Sherri J.
 ; TITLE OF INVENTION: Methods for controlling gibberellin levels

; FILE REFERENCE: MOBT:216
 ; CURRENT APPLICATION NUMBER: US/09/371,307A
 ; CURRENT FILING DATE: 1999-08-10
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 62
 ; LENGTH: 1359
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-09-371-307-62

Query Match 67.8%; Score 893.8; DB 3; Length 1359;
 Best Local Similarity 84.9%; Pred.No. 1.7e-250;
 Matches 1069; Conservative 1; Mismatches 158; Indels 31; Gaps 5;

QY 65 ACCATGGTTGTTCTGTCTCAGCAGCATTTGAACCACTTTTCTCTGAAACCAATTCAG 124
 DB 99 ACCATGGTTGTTCTGTCTCAGCAGCATTTGAACCACTTTTCTCTGAAACATGCAAG 158
 QY 125 TCACGCCCTTGTTCACGGGGATTCCTGTGTGCGACCTCAGCACCCCGATGCCAAGAT 184
 DB 159 CCCAGCCCTTGTTCGCGGGGATTCCTGTGTGCGACCTCAGCACCCCGATGCCAAGACC 218
 QY 185 CTCATAGTCAACGCGGTAGGACCTTCGGCTTCTCAAGCTTGTGAACCATGCTGTCCA 244
 DB 219 CACATAGTCAATGCTTCGCGGGGACTTCGGCTTCTCAAGCTGTAACCATGCTGTCCG 278
 QY 245 TTGGAGTTAATGGCCAAATTTAGAAACGAGGCGCTCAGGTCTTTTAAATAATCTCAGTCC 304
 DB 279 TTACAGTTTCAATGGCCAAATTTGAAACGAAACCTTCGGGTTCTTCAAAAAACCTCAATCC 338
 QY 305 GAGAAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGGTAGCAAGAGGATTTGGCCCA 364

DB 339 GAGAAAGACAGGGCTGTCCCTGACCCCTTTTGGCTAGGAGCAAGAGGATTTGGCCCT 398
 QY 365 AACCGTGTATGTCGGTTGGGTGGAATACCTCTCTCAACACCAACCTCTGATTTATCTCA 424
 DB 399 AACGCGATGTCGGTTGGGTGGAATACCTCTCTCAACACCAACCTCTGATTTATCTCC 458
 QY 425 CCCAAATCATTGTCATTTTCGAGAAAATCTCTCATCATTTTCAGGCGGTTGTCAGAAC 484
 DB 459 CCCAAGTCACTAGTTTCATTTTCAGAGAGGTCCTCAGAAATTTTCAGGCGGTTGTCAGGAA 518
 QY 485 TACATTACAGCAGTGAAGAACATGTCGTGTCGGTGTGGAAATTCATGCGCGAGGGTTG 544
 DB 519 TACATTAGAGCGGTGAAGAACATGTCGTATGAGGTGTGGAAATTCATGCGTCAGGAGTTG 578
 QY 545 GGGATAAGGCGAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGC 604
 DB 579 GGGATAAGCAGAGGAAATGTTGTTGAGTAGTGTGCTGAAGGATGAGAGAGTGTATCTTGC 638
 QY 605 TTCAGGTTGAACCACTACCCGCTTGGCTGAGTGCGTGAAGGCTGAACCTGAAC---CGGAATTTG 661
 DB 639 TTCAGACTTAACCACTACCCGCTATGCGCGGAGTGCAGGCAATTCAGCGAAGGAAATTTG 698
 QY 662 GTTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGCTCTAAGATCTAACAGCACCA 721
 DB 699 GTTGGATTTGGAGAGCACACAGACCCACAGATAATTTCTGCTTGAGATCTTAACAGCACCC 758
 QY 722 TCTGGCTTGCAAATCTGCTCACAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACT 781
 DB 759 TCAGGCTTGCAAATCTGCTCACAGATGGCACTTGGGTTTCTGCTCCCACTGATCAAACT 818
 QY 782 TCCTTTTTCATCAATGTTGGTGACGCTCTACAGTGAATGACTTAATGCGGAGGTTTAAAGT 841
 DB 819 TCCTTTTTCATCAATGTTGGTGACACTCTTTCAGGTAATGACTTAATGCGGAGGTTTAAAGT 878
 QY 842 GTAAAGCATAGGTTTTCGCTGACACACAGAGTCAAGGTTTATCAATGATCTACTTTGGA 901
 DB 879 GTAAAGCATAGAGTTTTCGCTGACCCCAACCAAGTCAAGGTTGCAATGATCTACTTTGGA 938
 QY 902 GGACCAAGGCTTGAAGTGAATAATAGCACCTTTTACCTTTCAGTGTATTAAGAGGAGAGAG 961
 DB 939 GGACCAAGGCTTGTGTGAAGATAGCACCTTTTACCTTTCATCTCATGTAAAGAGAGAGAG 998
 QY 962 TGTGTTGTAACAAAGAGTTCATGTTGTAATACAAAGAGGCTGCTGATCACTTCAAGGCTA 1021
 DB 999 AGTTTCTACAAAGAGTTCATGTTGGTGGGAATACAAAGAGGCTGCTGATCGCGTCAAGGCTA 1058
 QY 1022 GCTGATAATAGGCTTGGCCCTTCCAGAAATCTGCTGCTGATTAACCAACACACCCCTTC 1081
 DB 1059 GCGGATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGATTAAGAGGCAAGTGTGT 1118
 QY 1082 AAA-----TTCACCTCATTTTACGCACTGTTTATTAACCCCAA-----TTTTCTTTCTTTT 1132
 DB 1119 CAAATTTCTACTACTCAATTTTGGCAGCTGTTGTTAGGCCAACTTTTATTTTATTTT 1178
 QY 1133 TCTTTTCTGCTGCTGTAGGTTTCAACAGTTCATCTACTTGCATATATATAGAAAAT 1192
 DB 1179 TTTTGGGTGTGTATCTAGGTTCCAAACAGTTCATCTTACTTGCAGATATATAGAAAAT 1238
 QY 1193 GAATAGGT-----TAAGATGTTTATCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1241
 DB 1239 GAATAGGTGCTTATGACACTTCCCTTTTAAATCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1298
 QY 1242 TAAACAGTGGTCTCAACTTCCCTTTTCAATTTGCAATGGAACGCAACTCTAGTTTACA 1300
 DB 1299 TAATAGT-----CACTACTGCCCTTCTATTAATGAACGCAACTCTAGTTTACA 1349

RESULT 4

US-10-401-321-62
 ; Sequence 62, Application US/10401321
 ; Publication No. US20030233679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Sherri M.

<p> ; APPLICANT: Heck, Gregory R. ; APPLICANT: Pillier, Kenneth J. ; APPLICANT: Kilshore, Ganesh M. ; APPLICANT: Elich, Tedd D. ; APPLICANT: Logusch, Eugene W. ; APPLICANT: Rao, Sudabathula ; APPLICANT: Ream, Joel E. ; APPLICANT: Logusch, Sherry J. ; APPLICANT: Baerson, Scott R. ; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels ; FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1) ; CURRENT APPLICATION NUMBER: US/10/401,321 ; CURRENT FILING DATE: 2003-03-27 ; NUMBER OF SEQ ID NOS: 89 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 62 ; LENGTH: 1359 ; TYPE: DNA ; ORGANISM: Glycine max US-10-401-321-62 </p>		<p> Query Match 57.8%; Score 893.8; DB 6; Length 1359; Best Local Similarity 84.9%; Pred. No. 1.7e-250; Matches 1069; Conservative 1; Mismatches 158; Indels 31; Gaps 5; </p>	
QY	65	ACCATGGTGTCTGCTCAGCCAGCATTTGAACCCAGTCTTCTCTGAAACCATTTCAAG	124
Db	99	ACCATGGTGTCTGCTCAGCCAGCATTTAACCAGTCTTCTCTGAAACCATTTCAAG	158
QY	125	TCACGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCAGCACCCCGATGCCAAGAT	184
Db	159	CCACGCCCTTGTTCGGGGATTCCTGTGGTGCACCTCAGCACCCCGATGCCAAGACC	218
QY	185	CTCATAGTGAACCGCTGAGGACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTCCA	244
Db	219	CACATAGTCAATGCCCTGCGGGACTTCGGCTTCTCAAGCTCGTGAACCAACCGTGTTCGG	278
QY	245	TTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTCTCTTAAAAAATCTCAGTCC	304
Db	279	TTACAGTTTCATGGCCAAATTTGAAAACGAAACCTCGGGTCTTTCAAAAACCTCAATCC	338
QY	305	GAGAAAGACAGAGCTGGTCCCCCGACCCCTTTGGCTATGGTAGCAAGAGGATTGGCCCA	364
Db	339	GAGAAAGACAGAGCTGGTCCCCCGACCCCTTTGGCTACGGCAGCAAGAGGATTGGCCCT	398
QY	365	AACGGTGTGTGGTGGTGCATACCTCTCTCAACCAACCCCTGATGTTATCTCA	424
Db	399	AACGGCGATGTGGTGGTGCATACCTCTCTCAACCAACCCCTGATGTTATCTCC	458
QY	425	CCCAATCACTTTGCAATTTTCCGAGAAATCCTCATCATTTTCAGGGCGGTGGTGAAGAAC	484
Db	459	CCCAATCACTTTGCAATTTTCCGAGAAATCCTCATCATTTTCAGGGCGGTGGTGAAGAA	518
QY	485	TACATTACAGCAGTGAAGAACATGTCTATCGGGTGTGGAAATGATGCGGAGGGGTTG	544
Db	519	TACATTACAGCAGTGAAGAACATGTCTATGAGTGTGTGGAATGATGCTGAGGGATTG	578
QY	545	GGGATTAAGCAGAGGAATAGTTAACAGGTTGCTGAAGGATGAGAAAAGTGAATCGTGC	604
Db	579	GGGATTAAGCAGAGGAATAGTTAACAGGTTGCTGAAGGATGAGAAAAGTGAATCGTGC	638
QY	605	TTTCAGGTTCGAACCACTACCGCCCTTCCTGAGGTGCAAGCACTGAAC--CGGAATTTG	661
Db	639	TTTCAGGTTCGAACCACTACCGCCCTTCCTGAGGTGCAAGCACTGAACCGAAGGAATTTG	698
QY	662	GTTCGGTGTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACA	721
Db	699	GTTCGGTGTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACC	758
QY	722	TCGGCTTTCGAATCTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACT	781
Db	759	TCAGGCTTTCGAATCTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACT	818

RESULT 5

US-10-670-454-7
; Sequence 7, Application US/10670454
; Publication NO. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-7

Query Match 32.3%; Score 425.8; DB 8; Length 1237;
Best Local Similarity 66.3%; Pred. No. 2.4e-113;
Matches 629; Conservative 0; Mismatches 317; Indels 3; Gaps 1;
QY 146 ATTCTGTGGTGCAGCTCAGCACCCCGATCGGAAGCGAAACCCGAATCGTAAAGCCCTGCGAG 205
Db 199 ATCCCGGTGTCAACTAGCCGATCGGAAGCGAAACCCGAATCGTAAAGCCCTGCGAG 258


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QY 206 GACTTCGGCTTCTCAAGCTTGTAACCAAGTGTTCATGTGAGTTAATGCGCAATTTA 265
Db 259 GAGTTCGGCTTCTCAAGCTTGTAACCAAGTGTTCATGTGAGTTAATGCGCAATTTA 318
QY 266 GAAACGAGGCTTCAAGCTTGTAACCAAGTGTTCATGTGAGTTAATGCGCAATTTA 325
Db 319 GAGCAGGAGCTTCAAGCTTGTAACCAAGTGTTCATGTGAGTTAATGCGCAATTTA 378
QY 326 CCCGACCTTTCGGCTTATGTAAGAGGATTTGGCCCAAGGATGTCGGTTGGGTC 385
Db 379 CTTGAACCGTATGTAAGAGGATTTGGCCCAAGGATGTCGGTTGGGTC 438
QY 386 GAATACCTCTCTCAACCAAGGATTTGGCCCAAGGATGTCGGTTGGGTC 445
Db 439 GAGTATCTCTCTCAACCAAGGATTTGGCCCAAGGATGTCGGTTGGGTC 498
QY 446 CGAGAAATCTCTCAACCAAGGATTTGGCCCAAGGATGTCGGTTGGGTC 505
Db 499 CGTCAACCTCTCTCAACCAAGGATTTGGCCCAAGGATGTCGGTTGGGTC 558
QY 506 ATGTGCTATGCGGTGTTGGAATTTGATGGCGGAGGAGTGGGATAGGCGAGGAAATAG 565
Db 559 GTGTGCTACAGGTTGAGATGTTGCGGAGGATGTTGCGGAGGATGTTGCGGAGGAT 618
QY 566 TTAAGCAGGTTGCTGAAGGATGAGAAAGTGTGCTGCTTCAAGGATGTTGAGTACCG 625
Db 619 CTGAGTAAATGCTGAGAGATGAGAAAGTGTGCTGCTTCAAGGATGTTGAGTACCG 678
QY 626 CTTGCGCTGAGTGAACCAAGGATTTGGCCCAAGGATGTTGCGGATAGGCGAGGAA 685
Db 679 GCG--GCGGAGGAGGAGGAGGATGTTGCGGATAGGCGAGGAAATAG 735
QY 686 CCACAGATATTTCTGCTTAAGATCTAAGCAGCAGATCTGGCTTGCAGATCTGCTACA 745
Db 736 CCACAGATATTTCTGCTTAAGATCTAAGCAGCAGATCTGGCTTGCAGATCTGCTACA 795
QY 746 GATGCACTTGGGTTTCACTCCCACTGATCAGATCTCTTTTCAATCAATGTTGGTAC 805
Db 796 GATGGAAGTTGGTCTGCTCTGCTGATCACTCTCTTCTTCTTCAATGTTGGAGAT 855
QY 806 GCTTACAGTATGATGATGAGGATTTAAAGTGAAGCATAGGTTTGGCTGAC 865
Db 856 GCTCTTCAAGTTATGATGATGAGGATTTAAAGTGAAGCATAGGTTTGGCTGAC 915
QY 866 ACAACGAGTCAAGGTTTCAATGATCTACTTGGAGGACGAGTGTGAGTGAAGTATA 925
Db 916 ACAGAGATGAGGATTTCAATGATCTACTTGGAGGACGAGTGTGAGTGAAGTATA 975
QY 926 GCACCTTTACCTTCACTGATGTTTAAAGGAGGAGTGTGTTGTACAAAGATTCATGG 985
Db 976 GCACCATTTGCCATGCTTGTCTGAGCAAGATGATTTGCTTTTACAAAGATTCATGG 1035
QY 986 TGTGAATACAGAGGCTGCTGATCACTTCAAGCTAGCTGATTAATAGGCTTGGCCCTTC 1045
Db 1036 TCTCAATACAAATCTTCTGCTTCAAGCTTCAAGCTTGGTGTATAGACTTGGTCTCTTT 1095
QY 1046 CAGAAATCTGCTGATTTAAACCAACCAAGGATTTGAGTGAAGTGTATGAGTGTAT 1094
Db 1096 GAGAAACAACTTCTTCAATCAATAAAACCTTGTATGAGTGTATGAGTGTAT 1144

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RESULT 6

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US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Haiper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3

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; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1350
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1350

Query Match      32.3%; Score 425.4; DB 3; Length 1026;
Best Local Similarity 66.8%; Pred. No. 2.8e-113;
Matches 622; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

QY 146 ATTCTGTGGTCGACCTCAGCACCCGATCGATCGAAGAAATCTCATATAGTGAAACGCTGTAGG 205
Db 91 ATCCCGTCTTCAAGCTTGTGAACCATGGTGTTCATTTGGATTTAATGCGCAATTTA 265
QY 206 GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTTGGATTTAATGCGCAATTTA 265
Db 151 GAGTTTCGGGTTCTTCAAGGTCGTAAACCAACGAGGTCGACCCGAACTCATGACTCGGTTA 210
QY 266 GAAACGAGGCGCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGTGCTCC 325
Db 211 GAGCAGGAGGCTTATTTGGCTTCTTTCGGCTTGCCTCAGTCTCTTAAAAACGCGCTGCA 270
QY 326 CCCGACCTTTTCGGCTATGTAAGAGGATTTGGCCCAAGGATGTCGGTTGGGTC 385
Db 271 CTTGAACCTGTCGGTTATGTTAAATTAACGATTTGACCAACGATGACGTTGGTGGATT 330
QY 386 GAATACCTCTCTCTCAACCAACCCCTGATGTTATCTCACCACCAATCATTTTGCATTTTC 445
Db 331 GAGTATCTCTCTCTCAATGCTAATCTCAGCTCTCTCTCTTAAAAACCTTCCCGCTTTTC 390
QY 446 CGAGAAATCTCTCATCATTTTCAAGGCGGTGGTGGAGAACTACATTTACAGCAGTGAAGAAC 505
Db 391 CTTCAACCTCTCAATTTTTCGGTGTGCTGGTGGAGGATACATGAGGAGATTAAAGAA 450
QY 506 ATGTGCTATGCGGTTTGGAAATTTGATGCGGAGGAGTGGGATAGGCGAGGAAATAGC 565
Db 451 GTGTGCTCAAGGTTTGGAGATGTTGCGAAGAACTAGGATAGAGCAAGGACACT 510
QY 566 TTAAGCAGGTTGCTGAAGGATGAGAAAGTGTTCGTCGTTTCAAGCTTGAACCACTACCG 625
Db 511 CTGAGTAAATGCTGAGAGATGAGAAAGTGTGCTGCTGAGACTAAACCATTTATCCG 570
QY 626 CTTGCGCTGAGTCAAGCACTGAAACCGGAATTTTGGTTGGGTTTGGGAGCACACAGAC 685
Db 571 GC---GCGGAGGAGGAGGCGGAGAGATGTTGAGGTTGGGTTTGGGAGCACACAGAC 627
QY 686 CCACAGATAATTTCTGCTTAAAGATCTAACAGCAGCATCTGGCTTGCATAATCTGTCTACA 745
Db 628 CCACAGATAATTTCTGCTTAAAGATCTAACAGCAGGCTTTCATAATCTGTGTGAAA 687
QY 746 GATGCACTTGGGTTTCAAGCTTCAATGATCTACTTTGGAGGACCAAGGCTGTAGTGAAGTATA 925
Db 688 GATGGAAGTTGGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747
QY 806 GCTCTACAGGTAATGACTAATGAGGAGGTTTAAAGCTTAAAGCATAGGCTTTTGGCTGAC 865
Db 748 GCTCTTCAAGTTATGACTAAACGAGGAGTTCAGAGGTTTAAACACAGGCTCTTAGCCGAT 807
QY 866 ACAACGAGTCAAGGTTTCAATGATCTACTTTGGAGGACCAAGGCTGTAGTGAAGTATA 925
Db 808 ACAAGGAGATCGAGGATTTCAATGATATATTTTCGCGGAGCCGCCATTTGAGCCAGAGATC 867
QY 926 GCACCTTTACCTTCACTGATGTTTAAAGGAGGAGGATGTTTGTACAAAGATTCATCGG 985

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Db 868 GCACATTGCCATGCTGCTGCTGAGCAAGATGATTGGCTTTACAAAGAAATTCACCTGG 927

Qy 986 TGTGATACAGNAGGCTGGTACACTTCAAGCTAGCTGATTAATAGGCTTGCCCTTTC 1045

Db 928 TCTCAATACAAATCTTCTGCTTACAAAGTCTAAGCTTGGTGATTAAGACTTGGTCTCTTT 987

Qy 1046 CAGAAATCTGCTGCTGATTAACCAACACAC 1076

Db 988 GAGAAACACCTTCTCAATCATATAAACCC 1018

RESULT 7

US-09-938-842A-1350

; Sequence 1350, Application US/09938842A

; Publication No. US20040009476A9

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPT300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1350

; LENGTH: 1026

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1350

Query Match 32.3%; Score 425.4; DB 3; Length 1026;

Best Local Similarity 66.8%; Pred. No. 2.9e-113;

Matches 622; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

Qy 146 ATTCTGTGTGCTGACCTCAGCACCCCGATGCCAAGAATCTCATAGTGAACGCTCTAGG 205

Db 91 ATCCCGCTGCTCAACTAGCCGATCCGGAAGCAAAACCGATCTGAAGCCTCGAG 150

Qy 206 GACTTCGGCTTCTTCAAGCTTGGAACCATGTTGTTCCATTGGAGTTAATGGCAATTTA 265

Db 151 GAGTTCGGGTTCTTCAAGGTCGTAAACACCGAGTCCGACCGAACTCATGACTCGGTTA 210

Qy 266 GAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGNAAGACAGAGCTGGTCCC 325

Db 211 GAGCAGGAGCTATTGGCTTCTTTCGGCTTGCCCTCAGTCTTTAAAAACCGGGCCGCTCA 270

Qy 326 CCGACCCCTTTCGGCTATGTTAGACAGAGGATTGGCCCAACCGTGATGTCGGTTGGGTC 385

Db 271 CTGAACCGTAGCGTTATGGTATAAACCGATTGGACCAACCGTGACGTTGGTTGATT 330

Qy 386 GAATACCTCTCTCTCAACCAACCCCTGATGTTATCTCAACCCAAATCATTTCGATTTTC 445

Db 331 GAGTATCTCTCTCAATGTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 390

Qy 446 CGAAGAAATCTCATCATTTTCAGGCGGTGGTGAGAACTACATTACAGCAGTGAAGAAC 505

Db 391 CGTCAAAACCCCTCAATTTTTCGGTGAATCGGTGGAGGAGTACATGAAGGAGATTAAAGAA 450

Qy 506 ATGTGCTATCGGTGTTTGAATTTGATGGCGAGGGGTTGGGATAAGGCAGAGGAATACG 565

Db 451 GTGCTGACAGGTGTTGGAGATGTTGCCGAGAACTAGGATAGAGCCNAGGACACT 510

Qy 566 TTAAGCAGGTTGCTGAAGATGAGAAAGTATTCTGTTTCAAGTTGAAACCACTACCCG 625

Db 511 CTGAGTAAAAATGCTGAGAGATGAGAGAGTGAAGTCTGCTGCTGAGACTAAACCAATTATCG 570

Qy 626 CTTTGCCCTGAGTGCAGACACTGAACCGGAATTTTGGTGGTGGGAGCACACAGAC 685

Db 571 GC---GGCGGAGAGAGCGCGGAGAGATGGTGAAGTGGGTTTGGGGAACACACAGAC 627

Qy 686 CCACAGATAAATTTCTGTTTAAAGATCTAAACACACATCTGGCTTCAAAATCTGTCTACA 745

Db 628 CCACAGATAAATCTCAGTGTCTAAGATCTAATAACACGGGGGCTTTCMAATCTGTGTGAA 687

Qy 746 GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTTTTTCATCAATGTTGGTGAC 805

Db 688 GATGGAAGTTGGTGCCTGCTCCTCTGATCACTCTTCTTCTTCAATTAATGTTGAGAT 747

Qy 806 GCTCTACAGGTAATGACTAATCGGAGGTTTAAAGTGTAAAGCATAGGCTTTTGGCTGAC 865

Db 748 GCTCTTTCAGGTTATGACTAAACGGGAGGTTCAAGAGTGTAAACACAGGCTTTCAGCCGAT 807

Qy 866 ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAAGCGTTGAGTGAATAATA 925

Db 808 ACAAGGAGATCGAGGATTTCAATGATATATTTCCGGCGGACCGCCATTGAGCCAGAAGATC 867

Qy 926 GCACCTTTACCTTCAGTGTATGTTAAAGGAGAGGAGTGTTCATCAAAAGATTCACATGG 985

Db 868 GCACCAATTGCCATGCTTGTCCCTGAGCAAGATGATTGGCTTTTACAAAGAAATTCACCTGG 927

Qy 986 TGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCTTTC 1045

Db 928 TCTCAATACAAATCTTCTGCTTCAAGTCTAAGCTTGGTGATTAAGACTTGGTCTCTTT 987

Qy 1046 CAGAAATCTGCTGCTGATTAACCAACACAC 1076

Db 988 GAGAAACACCTTCTCAATCATATAAACCC 1018

RESULT 8

US-09-371-307-64

; Sequence 64, Application US/093711307A

; Patent No. US20020053095A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Sherri M.

; APPLICANT: Heck, Gregory R.

; APPLICANT: Piller, Kenneth J.

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Elich, Tedd D.

; APPLICANT: Logusch, Eugene W.

; APPLICANT: Rao, Sudabathula

; APPLICANT: Ream, Joel E.

; APPLICANT: Logusch, Sherry J.

; TITLE OF INVENTION: Methods for controlling gibberellin levels

; FILE REFERENCE: MOBT:216

; CURRENT APPLICATION NUMBER: US/09/371,307A

; CURRENT FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 1403

; TYPE: DNA

; ORGANISM: Glycine max

US-09-371-307-64

Query Match 32.2%; Score 424.8; DB 3; Length 1403;

Best Local Similarity 66.0%; Pred. No. 5e-113;

Matches 669; Conservative 0; Mismatches 327; Indels 18; Gaps 3;

Qy 53 ACAACAAACAAACCAACCATGTTGTTCTGCTCAGCCAGCAATGAACCAAGTTTTCCTTCTG 112

Db 134 AAAGCAGCAAGAAAAATGTTGTTGTTCTCAAGGCAACCAACAGAAACAATACTCTACATC 193

Qy 113 AAACCATTTCAAGTCCACGCCCTTGTTCAGCGGGATTCTCTGTCGACCTCAGCCACCCC 172

Db 194 AAGAACTACTGCCAACCGGCATTTCTCTCAACAAATTTCCCGTAGTGACCTCTCCAAACCA 253

Qy 173 GATGCCAAGAATCTCATAGTGAACGCCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAAC 232


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Db 254 GATGCAAGACCCCTCATAGTGAAGGCTTGTGAGGAATTTGGATCTTCAAAGTCATCAAC 313
Qy 233 CATGTGTTCCATTTGGAGTTAATGSCCAATTTAGAAAAGAGGCCCTCAGGTTCTTTAAA 292
Db 314 CATGGTGTCCCAATGAACTATATCCCAATTTGGAATCTGAAGCCCTTCAAGTCTTCTCT 373
Qy 293 AAATCTCAGTCGAGAGACAGAGCTGTGCTCCCGCCAGCCCTTTCCGGCTATGTTAGCAAG 352
Db 374 ATGCCACTCAATGAGAGGAAAAAGTAGGCCCTCCCAACCATATAGGGTATGTTAGCAAG 433
Qy 353 AGAATGGCCCAAAACGGTATGTCGGTGGGTGGAATACCTCTCTCTCAACCAACCCCT 412
Db 434 AAAATTTGACACAAATGGGGATGTGGTGGGTGAGTACCTTCTTCTCAACCAACCAATCAA 493
Qy 413 GATGTTATCTCACCCAAATCACTTTGCAATTTTCCGAGAAAATCCCTCATCATTTCAAGGG 541
Db 494 GAAACAACT-----TCTCTGTTTATGCAAAAACGCTGAGAAAATTTAGGTGT 541
Qy 533 GCGAGGGGTTGGGATTAAGGAGGAAATACGTTTAAAGCAGGTTGCTGAAGGATGAGAAA 592
Db 602 GCAGAGAGATTGAAGATACAAACAAAATGTTGTTAGCAAGCTTCTTATGATTAAGAG 661
Qy 593 AGTGATTCGTGCTCAGGTTGAAACCACTACCGCCCTTGCCTTGCCTGAGGTCGAAGCACTGAAC 652
Db 662 AGTGACTCTGTTTTAGGGTGAATCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
Qy 653 CGGAATTTGGTGGGTTGGGGAGCAGACAGACCCCAAGATATTTCTGCTTAAGATCT 712
Db 719 CAAAACATGATAGGGTTTGGAGAACACACGAGACCCCAAAATCATTTCTTCTACTAGGTCC 778
Qy 713 AACAGCATCTGGCTTGCATAATCTGCTCACAGATGGCAGCTTGGGTTTCAGTCCACCT 772
Db 779 AACATATCTTACGGCTTTCAGATTTTCTTAGAGATGGAATCTGATTTCACTCCACCT 838
Qy 773 GATCAGACTTCTTTTTTTCATCAATGTTGGTGAAGCTCTACAGGTAATGATTAATGGAGG 832
Db 839 GATCAGACTTCTTTTTCATCAATGTTGGTGAATCTTCTTCAAGGTTATGACCAATGGAAG 898
Qy 833 TTTAAAGTGTAAAGCATAGGCTTTGGCTGACACAAACGAGTCAAGGTTATCAATGATC 892
Db 899 TTTGCAAGTGTGAACACAGAGTTTGAACAATGGATTTAAGTCTAGACTCTCAATGAT 958
Qy 893 TACTTTGGAGGCCACCAATTTGAGTGAAGAAATATAGACCTTTTACCTTCAAGTGAATGTTAAA 952
Db 959 TACTTTGGAGGTCACCAATTTGAGTGAAGAAATATAGTACCAATTTTCACTTATG---AAA 1015
Qy 953 GGAGAGGAGTGTGTGACAAAGGTTTCATGTTGAGTGTGATACAGAGGCTCGGTACACT 1012
Db 1016 GGAAGAAAGCTTTATACAAAGAGTTTACGTGGTTCGAGTATAAAATTTAACCTTATGCT 1075
Qy 1013 TCAAGCTAGCTGATAATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGATTA 1066
Db 1076 TCAGAGTTGGCTGATTAATAGGCTTGACATTTTGAGAGAAATTTGTTGCTTCATA 1129
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RESULT 9

US-10-401-321-64

; Sequence 64, Application US/10401321

; Publication No. US2003023679A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Sherri M.

; APPLICANT: Heck, Gregory R.

; APPLICANT: Piller, Kenneth J.

; APPLICANT: Kileshore, Ganesh M.

; APPLICANT: Ellich, Redd D.

; APPLICANT: Logusch, Eugene W.

; APPLICANT: Rao, Sudabathula

; APPLICANT: Ream, Joel E.

```
; APPLICANT: Logusch, Sherry J.
; APPLICANT: Baerson, Scott R.
; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
; FILE REFERENCE: 11899.0216.DVUS01 (WOBT:216--1)
; CURRENT APPLICATION NUMBER: US/10/401,321
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-401-321-64
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Query Match 32.2%; Score 424.8; DB 6; Length 1403;
Best Local Similarity 66.0%; Pred. No. 5e-113;
Matches 569; Conservative 0; Mismatches 327; Indels 18; Gaps 3;
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Qy 53 ACAACAAACAACCATGTTGTTCTGCTCAGCAGCATTTGAACAGTTTTCCTCTG 112
Db 134 AAAGCAGCAAGAAAATGTTGTTGCTTCCAAGGCAACAACAGAAACAATACTCTACATC 193
Qy 113 AAACCATTCAGTCCACGCCCTTGTTCACGGGGATTTCTGTGTGACCTCAGCACCC 172
Db 194 AAGAACTACATGCCAACGGCATTTCTTCAACAATTCCTGAGTGGACTCTTCCAACCA 253
Qy 173 GATGCAAGAATCTCATAGTGAACCGCTGTAGGGAATTCGGCTTCTTCAAGCTTGTGAAC 232
Db 254 GATGCAAGACCTCATAGTGAAGCTTGTGAGGAATTTGGATTTCTTCAAGTCATCAAC 313
Qy 233 CATGTGTTCCATTTGGAGTTAATGSCCAATTTAGAAAAGAGGCCCTCAGGTTCTTTAAA 292
Db 314 CATGTGTTCCATTTGGAACTATATCCCAATTTGGAATCTGAAGCCCTTCAAGTCTTCTCT 373
Qy 293 AAATCTCAGTCGAGAAAGACAGAGCTGTGCTCCCGCCAGCCCTTTCCGGCTATGTTAGCAAG 352
Db 374 ATGCCACTCAATGAGAGGAAAATAGTGGCCCTCCCAACCAATATGTTAGTATGTTAGCAAG 433
Qy 353 AGGATTTGCCCAAAACGGTGTGTCGGTTGGGTGGAATACCTCTCTCTCAACCAACCACT 412
Db 434 AAATTTGACACAAATGAGGATGTTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 493
Qy 413 GATGTTATCTCACCAATCACTTTGCAATTTTCCGAGAAAATCCCTCATCATTTCAAGGG 472
Db 494 GAAACAACT-----TCTCTGTTTATGCAAAAACGCTGAGAAAATTTAGGTGT 541
Qy 473 GTGGTGGAGAACTACATTTACAGCAGTGAAGACATGCTGCTATGCGGTGTTGGAATTTGATG 532
Db 542 TTGTTGAACAGTTACATGCTTCTGTTGAGGAAAATGGCATGTTGAGATTTCTTGAAGTATG 601
Qy 533 GCGAGGGGTTGGGATTAAGGAGGAAATACGTTTAAAGCAGGTTGCTGAAGGATGAGAAA 592
Db 602 GCAGAGAGATTGAAGATACAAACAAAATGTTGTTAGCAAGCTTCTTATGATTAAGAG 661
Qy 593 AGTGATTCGTGCTCAGGTTGAAACCACTACCGCCCTTGCCTTGCCTGAGGTCGAAGCACTGAAC 652
Db 662 AGTGACTCTGTTTTAGGGTGAATCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
Qy 653 CGGAATTTGGTGGGTTGGGGAGCAGACAGACCCCAAGATATTTCTGCTTAAGATCT 712
Db 719 CAAAACATGATAGGGTTTGGAGAACACACGAGACCCCAAAATCATTTCTTCTACTAGGTCC 778
Qy 713 AACAGCATCTGGCTTGCATAATCTGCTCACAGATGGCAGCTTGGGTTTCAGTCCACCT 772
Db 779 AACATATCTTACGGCTTTCAGATTTTCTTAGAGATGGAATCTGATTTCACTCCACCT 838
Qy 773 GATCAGACTTCTTTTTTTCATCAATGTTGGTGAAGCTCTACAGGTAATGATTAATGGAGG 832
Db 839 GATCAGACTTCTTTTTCATCAATGTTGGTGAATCTTCTTCAAGGTTATGACCAATGGAAG 898
Qy 833 TTTAAAGTGTAAAGCATAGGCTTTGGCTGACACAAACGAGTCAAGGTTATCAATGATC 892
Db 899 TTTGCAAGTGTGAACACAGAGTTTGAACAATGGATTTAAGTCTAGACTCTCAATGAT 958
Qy 893 TACTTTGGAGGCCACCAATTTGAGTGAAGAAATATAGACCTTTTACCTTCAAGTGAATGTTAAA 952
Db 959 TACTTTGGAGGTCACCAATTTGAGTGAAGAAATATAGTACCAATTTTCACTTATG---AAA 1015
Qy 953 GGAGAGGAGTGTGTGACAAAGGTTTCATGTTGAGTGTGATACAGAGGCTCGGTACACT 1012
Db 1016 GGAAGAAAGCTTTATACAAAGAGTTTACGTGGTTCGAGTATAAAATTTAACCTTATGCT 1075
Qy 1013 TCAAGCTAGCTGATAATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGATTA 1066
Db 1076 TCAGAGTTGGCTGATTAATAGGCTTGACATTTTGAGAGAAATTTGTTGCTTCATA 1129
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206	QY	GACTTGGCTTCTTCAAGCTTGTGAACCAATGGTGTTCATTTGGAGTTAATGGCCAAATTTA	265
139	Db	GAGTTTGGGTCTTCAAAGTCATCAACCAATGGGGTCGGAACCCGATCTTTTGACTCAGTTG	198
266	QY	GA AAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC	325
199	Db	GAGCAAGAAGCCATCACTTCTTTTGCTTTGCATCACTCTCTCAAGAGACAAGCGGGTCCA	258
326	QY	CCGACCCCTTTCCGCTATGTGTAGCAAGAGAGATTGGCCCAAAACGGGTGATGTTCGGTTGGGTC	385
259	Db	CCTGACCCGTTTGGTTACGGTACTTAAAGAGATTGGACCAATGTGTGACCTTGGCTGGCTT	318
386	QY	GAATACCTCTCTCTCAACACCAACCCCTGATGTATTATCTCACCCAAATCACTTTTGCATTTTC	445
319	Db	GAGTACATTTCTCTTAATGTCTATCTTTTGCTTGAGTCTCACA AAAACCAACCGCCATTTTC	378
446	QY	CGAGAAATCCTCATCATTTTCAGGGCCGGTGGAGAACTATATTACAGCAGTGAAGAAC	505
379	Db	CGGCACACCCCTGCAATTTTTCAGAGAGCGCAGTGGAGAGTACATTAAGAGATGAAGAGA	438
506	QY	ATGTGCTATCGGGTTTGGAAATTGATCGCGAGGGGTTGGGGATAAGCCAGAGGAATACG	565
439	Db	ATGTGCGAGCAAAATTTCTGGAAATGGTAGAGGAGAGGCTTAAAGATAGAGCCAAAGGAGA	498
566	QY	TTAAGCAGGTTGCTTGAAGAGTGA AAAAGTGAATTCGTGCTTTTCAGGTTGAACTACCTCCG	625
499	Db	CTGAGCCGTTTGGTGAAAGTGAAGAAGTGAATTCGTGCTCGTGAATGAACCATTAACCG	558
626	QY	CTTTGCCCTCAGGTGCAAGCACTGAAACCGGAATTTGGTTGGGTTTGGGAGCACACAGAC	685
559	Db	-----GAGAAGGAAGAGACTCCCGGTCAAGGAAGAGATTGGGTTTCGGTAGCACACTGAT	612
686	QY	CCACAGATAATTTCTGTCTTAAGATCTAACAGACACATCTGGCTTTGCAAACTCTGTCTACA	745
613	Db	CCAAGTTGATATCACTGTCTCAGATCAAAACGACACAGAGGTTTGC AAACTCTGTCTCAA	672
746	QY	GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTTTTCATCAATGTTGGTGAC	805
673	Db	GATGGAACTAGGGTTGATGTATTACACCTGATCACTCTCTTTCTTTCTTTGTCGGAGAT	732
806	QY	GCTCTACAGGTATGACTTAATGGCAGGTTTAAAGTGTAAAGCATAGGTTTTCGGCTCAC	865
733	Db	ACTCTTCAGGTGATGACAAACGGAAGATTCAAGAGTGTGAACAATAGAGTGGTGACAAAT	792
866	QY	ACAAACGAAGTCAAGGTTTATCAATGATCTACTTTTCGAGGACACAGCGGTTTCAGTGA AAAATA	925
793	Db	ACAAAGGTC AAGGATATCGATGATCTACTTTCGCAGGTCCTCTCTTTGAGCGAGAAGATT	852
926	QY	GCACCTTACCTTCAGTGATGTTTAAAGGAGAGAGAGTGTTTGTACAAAAGTTCACATGG	985
853	Db	GCACCAATTATCATGCCCTTGTGCCAAAGCAAGATGATTGCCCTTTTATAATGAGTTTACTTGG	912
986	QY	TGTGAATACAAGAGGCTGCGTACACTTCAAGGCTAGCTGATATAAGCTTGCCTTTC	1045
913	Db	TCTCAATACAAGTTATCTGTCTTACAAAACACTAAGCTTGGTGACTATAGGCTTGGTCTCTTT	972
1046	QY	CAGAAATCTGCTGCTGATTAACAAAACA	1073
973	Db	GAGAAACGACCTCCATTTTCTCTATCCA	1000

RESULT 12	
US-10-670-454-5	
; Sequence 5, Application US/10670454	
; Publication No. US20040229357A1	
; GENERAL INFORMATION:	
; APPLICANT: Thomas, Stephen G	
; APPLICANT: Hedden, Peter	
; APPLICANT: Phillips, Andrew L	
; TITLE OF INVENTION: Gibberellin 2-Oxidase	
; FILE REFERENCE: 0623.0970000	
; CURRENT APPLICATION NUMBER: US/10/670,454	
; CURRENT FILING DATE: 2003-09-26	

Db 795 TGAGGCATAGGGTTTGTAGCTAACTGTAATAAATACTAGGGTTTCTATGATTTACTTCCGCTG 854
Qy 903 GACCAGCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGATGTTTAAAGAGGAGGAGT 962
Db 855 GACCTTCATTGACTCAGAGAATCGCTCCGTTGACATGTTTGAATGACAAATGAGGACGAGA 914
Qy 963 GTTTGTACAAAGAGTTTACATGCTGTGTGAATACAAAGAGGCTGGTACACTTCAAGGCTAG 1022
Db 915 GGTGTGACGAGGATTTACTTGTCTGAATACAAAACCTCTACTTAACTCTAGATTGT 974
Qy 1023 CTGATATAGGCTTGCCCTTTCCAGA 1049
Db 975 CTGATATAGGCTTCAACAATTCGAAA 1001

RESULT 13
US-10-392-325-3
; Sequence 3, Application US/10392325
; Publication No. US20040060080A1
; GENERAL INFORMATION:
; APPLICANT: Tanaka, Hiroshi
; APPLICANT: Kayano, Toshiaki
; APPLICANT: Matsuoka, Makoto
; APPLICANT: Kobayashi, Masatomo
; APPLICANT: Saito, Tamio
; APPLICANT: Sakamoto, Tomoaki
; APPLICANT: Sakai, Miho
; TITLE OF INVENTION: GIBBERELLIN 2-OXIDASE GENE, FUNCTIONS AND USES THEREOF
; FILE REFERENCE: SH2-014
; CURRENT APPLICATION NUMBER: US/10/392,325
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 7
; PRIOR APPLICATION NUMBER: JP 2002-276051
; PRIOR FILING DATE: 2002-09-20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
; OTHER INFORMATION:
US-10-392-325-3

Query Match 26.9%; Score 354; DB 7; Length 984;
Best Local Similarity 60.9%; Pred. No. 2.3e-92;
Matches 598; Conservative 0; Mismatches 375; Indels 9; Gaps 1;
Qy 69 TGGTTGTTCTGCTCAGCCAGCATTTGAACAGTTTTCCTTCGAAACCATTCAGTCCA 128
Db 5 TGGTTCTGCTGCGCCGCGCGTGCATCAGTCCCGTGTGAGGTCCGCGGACCCCG 64
Qy 129 CGCCCTTGTTCAGGGGATTCCTGTGTGCTCGACCTCAGCACCCCGGATGCCAAGAATCTCA 188
Db 65 GCGACGTCTTCTCGGGGTGCGGTGCTCGACCTCGCAGCCCGCGGGCGAGGGCCG 124
Qy 189 TAGTGAACCGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCAATGTTTCCATTGG 248
Db 125 TGGTGACGCTCGGAGCGGTACGGTCTTCAAGTGTGTCACACCGGCTGGCCACGG 184
Qy 249 AGTTAATGCCAATTTAGAAAACGAGCCCTCAGGTTCTTTAAATAATCTCAGTCCGAGA 308
Db 185 ACAGATGACAAGGCGGAGTCCGAGGCGGTGAGGTCTCAGGTTCTTCTCCAGAGCGAGCCGACA 244
Qy 309 AAGACAGAGTGTTCCTCCCGGACCTTTTCGGCTATGTTAGCAAGAGGATTTGGCCCAAAG 368
Db 245 AGGACCGCTCCGCGCCGCGCTACCGTTCCGGTACGGCAGCAGCGATCGGGTTCAATG 304
Qy 369 GTGATGTCGGTTGGGTGGAATACCTCTCTCAACACCAACCCCTGATGTTATCTCAACCA 428
Db 305 GCGACATGGGGTGGTTCGAGTACCTCTCTCTCGCCCTCGACGACGCGGTGCTGCGCGAG 364

Qy 429 AATCACTTTTGCATTTTCCGAGAAATCCCTCATCTTTCAGGCGGTGTTGGAGAACTACA 488
Db 365 CTGACACCGTCCGCTCTGCG-----CGGTCTTCCGGGCGGCTCTGACGAGTACA 415
Qy 489 TTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAATTTGATGCGGAGGGGTTGGGGA 548
Db 416 TCTCGGGGTGCGGAAGGTGGCGGTGATGAGGCGGATGTGCGAGGGGCTGGGCA 475
Qy 549 TAAGGACAGAGGAATAGCTTTAACGAGGTGCTGAAGATGAGAAAAGTGAATTCGTGCTTCA 608
Db 476 TTGCGCAGGCGGACCGCGCTGAGCGCTGCTGACGCGGAAGGAGCGACCAAGGTGTTCC 535
Qy 609 GGTGAACCACTACCCGCTTCCCTGAGGTGCAAGACTGAAACCGGAATTTGGTTGGGT 668
Db 536 GCGTGAACCACTACCCGCTGCGCGCTGCGAGGGGTGCGCTGCAGCGCTCACCGGCT 595
Qy 669 TTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACACACATCTGGCT 728
Db 596 TCGGCGAGCACACCGACCGCAGCTGCTCCGTGCTCCGCTCAACCGCACGTCGCGCC 655
Qy 729 TGCATATCTCTCACAGATGGCAGCTTGGGTTTCAGTCCCACTGATCAGACTTCCTTTT 788
Db 656 TGCAGATCGCGTCCGCGACGCGCTGAGTGGGTGTCGCTGCGCTCCGACCGGACTTCCTT 715
Qy 789 TCATCAATGTTGTTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGC 848
Db 716 TGTCAACGTGCGGACTGTTGCGAGTTCTGACCAATGGGAGGTTCAAGACGTTGAAGC 775
Qy 849 ATAGGTTTGTGCTGACACAAAGTCAAGGTTATCAATGATCTACTTTGGAGGACGAG 908
Db 776 ACAGGGTGGTGCCACAGCCTAAAGTCTAGGGTTTCCCTTCACTACTTTGGAGGGCCAC 835
Qy 909 CGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTGTTAAAGAGGAGGAGTGTGTTGT 968
Db 836 CGTTAGCACAGAGGATTGCACCATTTGCCACAGCTGCTGGGGGAGGAGCAGAGCGCTGT 895
Qy 969 ACAAGAGTTACATGTTGTAATCAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATA 1028
Db 896 ACAAGAGTTACATGCGGATGAGTACAGAGGCTGCTTCAAAATCAGAGCTTGGAGACA 955
Qy 1029 ATAGGCTTGCCCTTTCCAGAA 1050
Db 956 ACAGGCTGGCCCGAGTTTGAGAA 977

RESULT 14
US-10-437-963-78659
; Sequence 78659, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 78659
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78444C.1
US-10-437-963-78659

Query Match		26.9%;	Score 354;	DB 7;	Length 1260;
Best Local Similarity		60.9%;	Pred. No. 2.6e-92;		
Matches 598;		Conservative 0;	Mismatches 375;	Indels 9;	Gaps 1;
QY	69	TGGTTGTTCTGTCAGCCAGCATTAACCAAGTTTCTCTCTGAAACCATTCAGTCCA	128		
DB	144	TGGTTCTCGTGGCCGCCCGCGTGCATCATCCCGTGTGAGGTGCGCGGACCCCG	203		
QY	129	CGCCCTTGTTCACGGGATTCCTGTGTGTCGACTCACGACCCCGATGCCAAGATCTCA	188		
DB	204	CGACGTCTCTCCGCGTGCCTGCTCGACTCGGCAGCCCGCGCGGGGCGG	263		
QY	189	TAGTGAACCTGTGAGGACTTCGCGTCTTCAAGCTGTGAAACCATGTTTCATTTGG	248		
DB	264	TGTTGACGCTTCGAGCGGTACGGGTCTTCAAGTGTCTCAACACGCGCGTGGCCACG	323		
QY	249	AGTTAATGCCAAATTTAGAAACAGAGGCTCTCAGGTCTTTTAAATAATCTCAGTCCGAGA	308		
DB	324	ACACGATGACAAAGCCGAGTCGGAGGCGTCAAGTCTTCTCCAGACGACGCCGAC	383		
QY	309	AAGACAGAGCTGGTCCCGCCCGACCTTTCCGCTATGTGTAGCAAGAGATTTGGCCCAACG	368		
DB	384	AGGACCGTCCGCGCGCGCTACCGTTCGGGTACGGCAGCAAGCGATCGGGTTCATG	443		
QY	369	GTGATGTCGGTGGGTGCAATACCTCTCTCAACACCAACCTGATTTATCTCACCCA	428		
DB	444	CGACATGGGGTGGCTCGAGTACCTCTCTCGCCCTCGACGACGCTCGCTCGCGCAGC	503		
QY	429	AATCACTTTGCAATTTCCGAGAAATCTCATCATTTTCAGGGCGGTGGGAGACTACA	488		
DB	504	CTGCAACCGTCCCGTCTCTGCG-----CGGTCTTCGGGCGCTCTGAAACGAGTACA	554		
QY	489	TTACAGCAGTGAAGAACATGTCTATGCGGTGTGGAATTTGATGCGGAGGGTGGGGA	548		
DB	555	TCTCGGGGTGCGAAAGTGGCGGTGCGGGTGTGAGGCGATGTGAGAGGGCTGGGCA	614		
QY	549	TAAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGATGAGAAAGTGAATCTGCTTCA	608		
DB	615	TTGCGCAGCGGACGCGCTGAGCGCTGTTGACGCGGAGGAGGACGACGAGTGTTC	674		
QY	609	GTTGAACCACTACCGGCTTCCCTGAGTGCAGACTGAAACCGGAATTTGGTTGGT	668		
DB	675	CGGTGAACCACTACCGCGGTGCGCGCTGCAAGGGCTCGGCTGCAAGCGTCAACGGCT	734		
QY	669	TTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACTCTGGCT	728		
DB	735	TGCGGAGCACACACGACCCGCGAGCTGCTCGTCTCGCTCAACCGCAGCTCGGCG	794		
QY	729	TGCAATCTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTTT	788		
DB	795	TGCAGATCGCGCTCCGCGACGGCCAGTGGGTGTCCGTGCTCCGCTCCGACCGGACTCTTCT	854		
QY	789	TCATCAATGTTGTCAGCGCTTACAGGTAACTGCTAATGGGAGGTTTAAAGTGTAAAGC	848		
DB	855	TGCTCAACGTCGCGGACTCTGTTGCAAGTTCGACCAATGGGAGGTTCAAGACGCTGAAGC	914		
QY	849	ATAGGTTTGGCTGCACACAAAGTCAAGGTTCATGATCTACTTTGGAGACACAG	908		
DB	915	ACAGGTTGTGCCCAACAGCCTAAAGTCTAGGGTTTCCTTCACTTCTTGGAGGCCAC	974		
QY	909	CGTTGAGTGAATAATPAGCACCTTTACCTTTCAGTGTATGTTTAAAGGAGGAGTGTGTTG	968		
DB	975	CGTTAGCACAGAGGATTCACCATTTGCCACAGCTGTCTGGGGAGGAGAGAGCGCTGT	1034		
QY	969	ACAAAGATTACATGTTGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCTGATA	1028		
DB	1035	ACAAGAGTTACATGGGATGAGTACAGAGGCTGCCTTACAAATCAAGGCTTGGAGACA	1094		
QY	1029	ATAGGCTTGCCTTCCAGAA	1050		
DB	1095	ACAGGCTGGCCCGATTGAGAA	1116		

RESULT 15		US-10-425-115-69575			
		; Sequence 69575, Application US/10425115			
		; Publication No. US20040214272A1			
		; GENERAL INFORMATION:			
		; APPLICANT: La Rosa, Thomas J.			
		; APPLICANT: Kovalic, David K.			
		; APPLICANT: Zhou, Yihua			
		; APPLICANT: Cao, Yongwei			
		; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
		; TITLE OF INVENTION: Plants			
		; FILE REFERENCE: 38-21(53222)B			
		; CURRENT APPLICATION NUMBER: US/10/425,115			
		; CURRENT FILING DATE: 2003-04-28			
		; NUMBER OF SEQ ID NOS: 369326			
		; SEQ ID NO 69575			
		; LENGTH: 1611			
		; TYPE: DNA			
		; ORGANISM: Zea mays			
		; FEATURE:			
		; OTHER INFORMATION: Clone ID: MRT4577_163444C.1			
		US-10-425-115-69575			
Query Match		24.0%;	Score 315.8;	DB 8;	Length 1611;
Best Local Similarity		58.9%;	Pred. No. 4.8e-81;		
Matches 586;		Conservative 0;	Mismatches 397;	Indels 12;	Gaps 2;
QY	59	ACAACAACCATGTTGTTCTCTCTCAGCCAGCATTTGAACCAAGTTTTCCTCTCTGAACCA	118		
DB	169	ACAGCATGTTGGTGTCTCGCCAAACCGCTGTCTGTCGACCAAGTCCCGCTCTCGGGTCC	228		
QY	119	TTCAAGTCCACGCCCTTTTTCACGGGGATTCCTGTGTGTCGACCTCACGACCCCGATGCC	178		
DB	229	CGGGCCCCAGGACAGCTTCTCGGAGTGCCTGCGTGTGACCTGTCTCAGCCACGCGCG	288		
QY	179	AAGAACTCATAGTGAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGACCATGGT	238		
DB	289	CGCGGGCGCATGCTCGACGCTTCGAGCGCTTCGGGTTCTTCAAGGTCTCAACCAACGCG	348		
QY	239	GTTCCATTTGAGTTAAATGGCCAAATTTAGAAAAAGAGGCGCTCAGGTTCTTTAAAAAATCT	298		
DB	349	GTGGCGGGCGCCACCATGGAAGAGGGCGAGTCCGAGGCGCTCAGGTTCTTCGGCAGGGG	408		
QY	299	CAGTCCGGAAGAAGACAGAGCTGGTCCCGCCGACCTTTCCGCTATGTGTAGCAAGAGATT	358		
DB	409	CAGCGGACAAAGGACCGCGCGGGCGCGGTACCGTTCCGGTACGCGCAGCAAGCGGATC	468		
QY	359	GGCCCAACCGGTGATGTCGGTTGGTTCGAATACCTCTCTCTCAACACCAACCCCTGATGT	418		
DB	469	GGGCTCAATGGCGACATGGGGTGGCTCGAGTACCTCTCTCTCGCGCTCGACGCGCGTGG	528		
QY	419	ATCTCACCCAAATCACTTTTGCAATTTTCGAGAAAAATCCTCATCTTCAGGGCGGTGGTG	478		
DB	529	CTCTCCGAGCGCTGCCCGCTCCAGCG-----CGCGTTCCGAGGCGCGCTG	579		
QY	479	GAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAATTTGATGCGGAG	538		
DB	580	AACGAGTACGTCGCGCGCTGCGGAAGGTGGCGCGCGTGTGCTGGAGCGGATGCGGAG	639		
QY	539	GGGTTGGGGAATAGGACAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAATGAT	598		
DB	640	GGCCTGGGCATTTGGCGACGCGGACGCGCTGAGCTCCATGTGTGAGCGCGCGCGGAGCGAC	699		
QY	599	TGCTGCTTCAGTTGAACCACTACCGCTTTCCTGAGGTGCAAGACTGAACCGGAAT	658		
DB	700	CAGGTGTTCCGCGTGAACCACTACCGCTTTCCTCCCGCGCTGACGGGCTGGGCTGACGC	759		
QY	659	TTGGTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGC	718		
DB	760	GCCAGGGCTTCGGCGACACACCGACCCGAGATCATCTCGTCTCGCTCCGCTCCCAACGCG	819		
QY	719	ACATCTGGCTTGCAAAATCTGTCTCAGATGGCAC---TTGGGTTTCAGTCCCACTGAT	775		

Db 820 ACCTCGGCTGCAGATCGGCTCCGGAACGGCGCAGTGGGTCTCCGTGCCCTCCGAC 879

Qy 776 CAGACTTCCTTTTTCATCAATGTGGTGACGCTCTACAGTAAATGAGGTTT 835

Db 880 CGCGACGCTTCTTCGTTAACGTGCGGACTCGTTGCAGGTGCTGACCAACGGGAGTTC 939

Qy 836 AAAAGTGTAAGCATAGGGTTTGGCTGACACAAAGTCAAGGTTATCAATGATCTAC 895

Db 940 AGGAGCGTGAAGCACCGGGTGGTGACCAACAGCCTCAAGTCCAGAGTTTCTTCATCTAC 999

Qy 896 TTTGGAGGACCAAGCTTGAGTGAATATAGCACCTTTACCTTCAGTGATGTTAAAGGA 955

Db 1000 TTGCGGGGCGCGCTGGGGCAGCGGATCGCGCGCTGCCGAGGTGCTGGCGGAGGA 1059

Qy 956 GAGGAGTGTGTGTAAGAGTTTACATGTTGTAATACAAGAGGCTGCTACACTTCA 1015

Db 1060 GAGGAGAGCTGTACAAGAGTTTCACTGGGGCGAGTACAAGAGCCCGGTACAGACG 1119

Qy 1016 AGGCTAGCTGATAATAGGCTTGCCCTTTTCCAGAA 1050

Db 1120 AGGCTCGGCGACAACAGGCTGGCCCAAGTTTGAGAA 1154

Search completed: December 28, 2005, 01:23:05
Job time : 1242.83 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 18:17:41 ; Search time 237.513 Seconds
(without alignments)
2879.764 Million cell updates/sec

Title: US-10-670-454-1
Sequence: 1318
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA New:
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

*red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	56.4	4.3	1017	US-11-152-892-5
2	40.8	3.1	3159	US-10-750-185-48573
3	40.6	3.1	164527	US-11-121-086-71
4	40	3.0	1011	US-11-152-892-3
5	39.2	3.0	3861	US-11-152-892-2
6	39.2	3.0	1125000	US-10-995-561-13286
7	38.8	2.9	150437	US-11-112-908-44
8	38.8	2.9	182314	US-11-112-908-45
9	38.6	2.9	130472	US-10-995-561-13312
10	38.4	2.9	1258	US-10-997-437A-1
11	37.4	2.8	4873	US-10-750-185-64795
12	37.2	2.8	201	US-10-995-561-52521
13	37.2	2.8	2555	US-10-750-185-53362
14	37	2.8	158410	US-11-121-086-46
15	36.8	2.8	1276	US-10-750-185-59293
16	36.8	2.8	3926	US-10-909-125-796
17	36.4	2.8	1688	US-10-750-185-31828
18	36.4	2.8	645179	US-10-995-561-13393
19	36.2	2.7	159497	US-11-112-908-61
20	36.2	2.7	166639	US-11-121-086-52
21	36	2.7	842	US-10-750-185-42851
22	36	2.7	2171	US-11-152-892-1
23	36	2.7	18059	US-10-995-561-13195

C 24	36	2.7	142605	7	US-11-121-086-64	Sequence 64, Appl
C 25	35.6	2.7	1778	6	US-10-750-185-37195	Sequence 37195, A
C 26	35.6	2.7	137935	6	US-10-995-561-13278	Sequence 13278, A
C 27	35.6	2.7	163317	7	US-11-117-187-212	Sequence 212, App
C 28	35.4	2.7	1229	6	US-10-750-185-57430	Sequence 57430, A
C 29	35.4	2.7	3720	6	US-10-927-641-127	Sequence 127, App
C 30	35.4	2.7	237326	7	US-11-157-389-2	Sequence 2, Appl1
C 31	35.2	2.7	1464	6	US-10-750-185-48102	Sequence 48102, A
C 32	35.2	2.7	1828	6	US-10-750-185-47560	Sequence 47560, A
C 33	35.2	2.7	1987	6	US-10-750-185-42377	Sequence 42377, A
C 34	35.2	2.7	40887	6	US-10-995-561-13303	Sequence 13303, A
C 35	35	2.7	1080	6	US-10-750-185-54120	Sequence 54120, A
C 36	35	2.7	3770	7	US-11-174-166-19	Sequence 19, Appl1
C 37	34.8	2.6	1126	6	US-10-750-185-34028	Sequence 34028, A
C 38	34.8	2.6	1082144	7	US-11-117-187-211	Sequence 211, App
C 39	34.6	2.6	162173	7	US-11-121-086-72	Sequence 72, Appl
C 40	34.6	2.6	175673	7	US-11-121-086-55	Sequence 55, Appl
C 41	34.4	2.6	1419	6	US-10-821-234-73	Sequence 73, Appl
C 42	34.4	2.6	3575	6	US-10-750-185-28226	Sequence 28226, A
C 43	34.4	2.6	169047	7	US-11-121-086-15	Sequence 15, Appl
C 44	34.2	2.6	1633	6	US-10-955-054A-103	Sequence 103, App
C 45	34.2	2.6	3454	6	US-10-793-626-4305	Sequence 4305, Ap

ALIGNMENTS

RESULT 1
US-11-152-892-5
; Sequence 5, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzeil, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296, 97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1014)
US-11-152-892-5

Query Match 4.3%; Score 56.4; DB 7; Length 1017;
Best Local Similarity 55.7%; Pred. No. 3.2e-06;
Matches 108; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY	741	TCACAGATGACCTTGGGTTTACGTCACCTGATCAGACTTCCTTTTCATCATGTTG	800
DB	704	TCAAGACATATGATGATCGCTGTTAACTTAATCTTAAGCTCTCATTAATCAATATG	763
QY	801	GTGAGCCTTACAGATTAAGTAAAGGAGTTTAAAGTGAAGCATAGGTTTGG	860
DB	764	GTGACTTATTTACGATGAGCAATGATGACAAAGTGTGAACCGGTATATA	823
QY	861	CTGACACAAAGATCAAGTTATCATATCTACTTTGAGAGCAGCGTTGAGTGAAA	920
DB	824	CGAACCAAAAGGAGGAGATTTCTAAGCGCTTATTTATGTGTCATCATACGAGCGG	883
QY	921	ATATGACCTTTA 934	
DB	884	TTATAGATGTTC 897	


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RESULT 2
US-10-750-185-48573/C
; Sequence 48573, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FATTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48573
; LENGTH: 3159
; TYPE: DNA
; ORGANISM: Bovine 19866880619350
; US-10-750-185-48573

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Query	Match	Similarity	Score	DB	Length
Best	Local	52.3%	Pred. No. 0.2;		
Matches	90;	Conservative	0;	Mismatches	82;
				Indels	0;
				Gaps	0;
QY	1046	CAGAAATCTGCTGTGATTAACCAACACACCCCTCAATTCACATCTATTTAAGCAGCT	1105		
Db	1298	CAGAACTTATATGCTATTAAGTACATTAATCTTTTAAAAATATCCGAAACTTCCAAACAG	1239		
QY	1106	GTTATTAACCAATTTTCTTTCCTTTTCTTTCTGTGCTGTCTAGAGTTCAACAGT	1155		
QY	1238	TTTCTTCTCTAAATATATTTTCATCTGTTTTCACAGCTGTATTTTGGTAAATAGACACT	1179		
QY	1166	TGACTTACTTGACATATATAGAAAATGAATAGTTAGATGTTATATATTT	1217		
Db	1178	TGAGCAAAATCTGGTTACTTTCATATATATATAGACATCACTATGTTCCAGATTT	1127		

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RESULT 3
US-11-121-086-71
: Sequence 71, Application US/11121086
: Publication No. US20050266459A1
: GENERAL INFORMATION:
: APPLICANT: NIELSEN, TIM S.
: APPLICANT: NIELSEN, KIRSTEN V.
: TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
: FILE REFERENCE: 09138.6000-00000
: CURRENT APPLICATION NUMBER: US/11/121.086
: CURRENT FILING DATE: 2005-05-04
: PRIOR APPLICATION NUMBER: 60/567,570
: PRIOR FILING DATE: 2004-05-04
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 71
: LENGTH: 164527
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-11-121-086-71

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Qy	1060	TGATTAAACCAACACACCCCTTGAATTCACATCTTTTACGACAGCTGTTATTAACCCCAAT	1119
Db	149090	TGCTTAAATTAATATGTAACAGTAACTTTTGCTATCTTTTAAGAAGTGGAGATTATATGTCGATT	149149
Query Match 3.1%; Score 40.6; DB 7; Length 16527;			
Best Local Similarity 52.0%; Pred. No. 2.4;			
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;			

[illegible]

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RESULT 4
US-11-152-892-3
Sequence 3, Application US/11152892
Publication No. US20050251883A1
GENERAL INFORMATION:
APPLICANT: Amsino, Richard M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Bizzell, Colleen M.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: US/11/152, 892
CURRENT FILING DATE: 2005-06-15
PRIORITY APPLICATION NUMBER: US/10/155,435
PRIORITY FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1011
TYPE: DNA
ORGANISM: Arabidopsis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1008)
US-11-152-892-3

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Query Match	3.0%;	Score 40;	DB 7;	Length 1011;
Best Local Similarity	53.1%;	Pred. No. 0.17;		
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Qy	747	ATGGCACTTGGGTTTCAGTCCCACTCATATCAGCTTCTTTTATCATANTGTGGTACG	806	
Db	713	ATGCACATATGATTCAGGGTAAACCTTGCTTGGAAAGCCCTTACAGTCAACTTTGGGATA	772	
Qy	807	CTTCAAGGTATATGACTTAATGGAGGTTTAAAGTGAACATAGGCTTTGGCTGACA	866	
Db	773	TGTTTCAGGCACTAGTATGAGAGTGAACCAACGATGACATATGATGATTTCTCCAG	832	
Qy	867	CAACGAAGTCAAGGTTTATCATATGATCTACTTTGGAGGACC	906	
Db	833	CAATATTCGAGAGGATGTCAATAGCTTTCTTCGATATGCC	872	

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RESULT 5-2
US-11-152-892-2
Sequence 2, Application US/11/152892
Publication NO. US20050251863A1
GENERAL INFORMATION:
APPLICANT: Amasino, Richard M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Michael, Scott D.
APPLICANT: Bizzell, Colleen M.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION NUMBER: US/10/155,435
PRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 3861
TYPE: DNA
ORGANISM: Arabidopsis

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DB 17 ATTTGTGATATATTTCTTGTCTGTCGCTGAATTTTACACATATGATCACTCAT 76
 QY 1178 ACATATATAGAAATGAATAGTTAGATGTTATCATTTCTTTCTTTGTTCACTCA 1237
 DB 77 CAATGATAGGTAAAGTTTCTTTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTG 136
 QY 1238 AGGTAAAGATTTGCTCAACTTCCC 1263
 DB 137 TTTGTGATGATGCTGCACTGCTC 162

RESULT 13

US-10-750-185-53362/C
 ; Sequence 53362, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 53362
 ; LENGTH: 2555
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880739412
 ; US-10-750-185-53362

Query Match 2.8%; Score 37.2; DB 6; Length 2555;
 Best Local Similarity 56.6%; Pred. No. 1.9;
 Matches 69; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1105 TGTATATACCCATTTCTTCTTTCTTCTTCTGTCGCTGATGTTCAACAG 1164
 DB 1843 TGTATATACCCATTTCTTCTTTCTTCTTCTGTCGCTGATGTTCAACAG 1784
 QY 1165 TTGACTTACTTACATATATAGAAATGAATAGTTAGATGTTATTCATTTCTTTT 1224
 DB 1783 ATATTTCTATTTCCACAGACTTCTATATATAATTTGTTCTTCTTATTTCTT 1724
 QY 1225 CT 1226
 DB 1723 TT 1722

RESULT 14

US-11-121-086-46
 ; Sequence 46, Application US/11121086
 ; Publication No. US20050266459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: POULSEN, TIM S.
 ; APPLICANT: NIELSEN, KIRSTEN V.
 ; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
 ; FILE REFERENCE: 09138.6000-00000
 ; CURRENT APPLICATION NUMBER: US/11/121,086
 ; CURRENT FILING DATE: 2005-05-04
 ; PRIOR APPLICATION NUMBER: 60/567,570
 ; PRIOR FILING DATE: 2004-05-04
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 46
 ; LENGTH: 158410
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-11-121-086-46

Query Match 2.8%; Score 37; DB 7; Length 158410;
 Best Local Similarity 54.9%; Pred. No. 26;
 Matches 73; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1021 AGCTGATATAGGCTGCCCCCTTCCAGAAATCTGCTGATTAACCAACACACCTT 1080
 DB 47020 AACATATATGACTTCTTATACCAAGACGTGTGACAGAAACAAATCTTACTT 47079
 QY 1081 CAATTCACATATTTAGCAGAGTGTATATACCCCAATTTCTTTCTTTTCC 1140
 DB 47080 CAAGCAACACCTTTGATATATATATATATGTCGAAGTTTCTTTTCTTTT 47139
 QY 1141 TGTGCTGCTAG 1153
 DB 47140 TTTTCTTTTTCAG 47152

RESULT 15

US-10-750-185-59293/C
 ; Sequence 59293, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 59293
 ; LENGTH: 1276
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866881070663
 ; US-10-750-185-59293

Query Match 2.8%; Score 36.8; DB 6; Length 1276;
 Best Local Similarity 55.5%; Pred. No. 1.6;
 Matches 71; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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 DB 494 TTGCTTTATTTGGTTGCTTTAGCATTTTATATTTAAACAAGTTTCTAAGATTTAA 435
 QY 1189 AATGATAGATTAAGATGTTATCATTTCTTTCTTTGTTTCACTTAAGTTAAAGT 1248
 DB 434 AATTTAATGATTAATTTATTTCTACCAATGTTTCTGATTCACCAATATATTAACAT 375
 QY 1249 TGGTCTCA 1256
 DB 374 TTATCTCA 367

Search completed: December 28, 2005, 01:30:10
 Job time : 242.513 secs

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		Match	Length			
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2	996	100.0	1318	6	BD243009	BD243009 Enzyme. 7
3	996	100.0	1318	6	AX444991	Sequence
4	996	100.0	1318	6	AX008671	Sequence
5	996	100.0	1318	15	POI32438	AUI32438 Phaseolus
6	920.8	92.4	1360	15	AB181372	AB181372 Vigna an
7	827.4	83.1	1359	6	AR528429	Sequence
8	483.8	48.6	1406	15	AY588978	AY588978 Nerium o
9	463.8	46.6	1245	15	AY594292	AY594292 Nerium o
10	461.2	46.3	1383	15	CWA315663	CWA315663 Cucurbit
11	458	46.0	1308	15	CWA302041	AYJ302041 Cucurbit
12	443	44.5	1292	15	AB125232	AB125232 Nicotiana
13	436	43.8	1479	15	MMY09113	Y09113 M. macrocar
14	424.4	42.6	1026	6	AX506655	AX506655 Sequence
15	424.4	42.6	1026	6	AX651428	AX651428 Sequence
16	424.4	42.6	1057	15	BT004464	BT004464 Arabidops
17	424.4	42.6	1223	15	AYH132436	AYJ132436 Arabidops
18	424.4	42.6	1237	6	BD243013	BD243013 Enzyme. 7

QY	181	GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	240		
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QY	241	AAAGCAGAGCTGGTCCCCCGACCCCTTTCCGCTATGTTAGCAAGAGGATTTGGCCCAAC	300		
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QY	301	GGTGATGTCGGTTGGTGCATATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCC	360		
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QY	361	AAATCACTTTGCAATTTCCGAGAAATCTCATCATTTTCAGGCGGTGTTGAGAACTAC	420		
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QY	901	TACAAAGAGTTACATGGTGTGAATACAAAGAGCGTGGTACACTTCAAGGCTAGCTGAT	960		
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LOCUS	BD243009				
DEFINITION	Enzyme.				
ACCESSION	BD243009				
VERSION	BD243009.1	GI:33052779			
KEYWORDS	JP 2002518005-A/1.				
SOURCE	Phaseolus coccineus				
ORGANISM	Phaseolus coccineus				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
	rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;				
	Phaseolus.				
REFERENCE	1 (bases 1 to 1318)				
AUTHORS	Thomas, S.G., Hedden, P. and Phillips, A.L.				

Enzyme	Patent: JP 2002518005-A 1 25-JUN-2002;	
JOURNAL	THE UNIVERSITY OF BRISTOL	
COMMENT	Phaseolus coccineus (scarlet runner bean)	
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PN	JP 2002518005-A/1	
PD	25-JUN-2002	
PF	11-JUN-1999 JP 2000554838	
PR	12-JUN-1998 GB 9812821.8,15-JUL-1998 GB 9815404.0 P1	
STEPHEN GREGORY THOMAS, PETER HEDDEN, ANDREW LEONARD PHILLIPS PC		
C12N9/04,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10,PC		
C12N15/09,		
PC C12N5/00,C12N5/00,C12N15/00		
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QY	61 AGCCCTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGCACCCCGATGCCAAGATCTC	120
Db		
QY	128 AGCCCTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGCACCCCGATGCCAAGATCTC	187
Db		
QY	121 ATAGTGAACGCGCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG	180
Db		
QY	188 ATAGTGAACGCGCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG	247
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QY	181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	240
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QY	248 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	307
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QY	301 GGTGATGTCGGTTGGTGCATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCC	360
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QY	368 GGTGATGTCGGTTGGTGCATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCC	427
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QY	361 AAATCACTTTGCAATTTCCGAGAAAATCTCATCATTTTCAGGCGGTGTTGAGAACTAC	420
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QY	428 AAATCACTTTGCAATTTCCGAGAAAATCTCATCATTTTCAGGCGGTGTTGAGAACTAC	487
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QY	601 TTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC	660
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QY	668 TTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC	727
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QY 901 TACAAGAGTTCACATGGTGTAATACAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
DB 968 TACAAGAGTTCACATGGTGTAATACAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
QY 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGAT 996
DB 1028 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGAT 1063

RESULT 3
LOCUS AR444991 1318 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6670527.
ACCESSION AR444991
VERSION AR444991.1 GI:42672879
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1318)
AUTHORS Thomas, S.G., Hedden, P. and Phillips, A.L.
TITLE Gibberellin 2-oxidase
JOURNAL Patent: US 6670527-A 1 30-DEC-2003;
The University of Bristol; Bristol;
GBX; Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 996; DB 6; Length 1318;
Best Local Similarity 100.0%; Pred. No. 2.2e-291;
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ACGCCCTTCTTCAAGGGATTCCTGTGGTGCACCTCAGCAGCCCGGATGCCAAGATCTC 120
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RESULT 4
AX008671
LOCUS AX008671 1318 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9966029.
ACCESSION AX008671
VERSION AX008671.1 GI:9996195
KEYWORDS
SOURCE Phaseolus coccineus
ORGANISM Phaseolus coccineus
REFERENCE 1
AUTHORS Phillips, A.L., Hedden, P. and Thomas, S.G.
TITLE Enzyme
JOURNAL Patent: WO 9966029-A 1 23-DEC-1999;
PHILLIPS ANDREW LEONARD (GB); HEDDEN PETER (GB); UNIV BRISTOL (GB);
THOMAS STEPHEN GREGORY (GB)
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Qy 901 TACAAAGAGTTCACATGTTGTAATACAAAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
Db 968 TACAAAGAGTTCACATGTTGTAATACAAAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
Qy 961 AATAGCTTGGCCCTTTCAGAAATCTGCTGAT 996
Db 1028 AATAGCTTGGCCCTTTCAGAAATCTGCTGAT 1063

RESULT 6
LOCUS AB181372 1360 bp mRNA linear PLN 09-JUN-2005
DEFINITION Vigna angularis VaGA2oxA1 mRNA for gibberellin 2-oxidase, complete cds.
ACCESSION AB181372
VERSION AB181372.1 GI:67077811
KEYWORDS Vigna angularis (adzuki bean)
SOURCE Vigna angularis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
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REFERENCE 1
AUTHORS Park,S., Nakajima,M., Xu,Z., Tomioka,K., Sakane,M. and Yamaguchi,I.
TITLE Gibberellin 2-oxidases from adzuki bean hypocotyl
JOURNAL Unpublished
2 (bases 1 to 1360)
REFERENCE 2
AUTHORS Nakajima,M., Xu,Z., Park,S., Tomioka,K., Sakane,M. and Yamaguchi,I.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2004) Masatoshi Nakajima, The University of

Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture; 1-1-1 Yayoi, Bunkyo, Tokyo, 113-8657, Japan
(E-mail:nkjm@gri.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192, Fax:81-3-5841-8025)
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Best Local Similarity 95.3%; Pred. No. 1.8e-268;
Matches 949; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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Db 143 ACGCCCTTTGTTACGGGGATTCCTGTGTGCGACCTCAGCACCCCGATGCCAAGATCTC 202
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RESULT 7
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LOCUS AR528429
DEFINITION Sequence 62 from patent US 6723897.
ACCESSION AR528429
VERSION AR528429.1 GI:53916494
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1359)
AUTHORS Brown,S.M., Elich,T.D., Heck,G.R., Kishore,G.M., Logusch,B.W.,
Logusch,S.J., Pillar,K.J., Rao,S., Ream,J.E. and Baerson,S.R.
TITLE Methods for controlling gibberellin levels
JOURNAL Patent: US 6723897-A 62 20-APR-2004;
Monsanto Technology, LLC; St. Louis, MO
FEATURES
source Location/Qualifiers
1..1359
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 83.1%; Score 827.4; DB 6; Length 1359;
Best Local Similarity 89.9%; Pred. No. 4.9e-240;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;
QY 1 ATGGTTGTTCTGTCTCAGCCAGCAATGACCACTTTTCTCTCTGAAACCAATTCAGATCC 60
Db 102 ATGGTTGTTCTGTCTCAGCCAGCAATTAACCACTTTTCTCTGAAACCAATTCAGATCC 161
QY 61 ACGCCCTTGTTCACGGGGATTCTGTGGTGCAGCTCACGCCACCCCGATGCCAAGAAATCTC 120
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QY 121 ATAGTGAACGCTGTAGGAGCTTTCGGCTTCTTCAAGCTTGTAACCATGTTTCCATTG 180
Db 222 ATAGTCAATGCTTCAGGGAGCTTTCGGCTTCTTCAAGCTTGTAACCATGTTTCCGTTA 281
QY 181 GAGTTAATGCCCAATTTAGAAACGAGGCCCTCAGGTTCTTTTAAANAATCTCAGTCCGAG 240
Db 282 CAGTTTCATGGCCAAATTTGGAACACGAAACCTCGGGTTCTTCAAAAACCTCAATCCGAG 341
QY 241 AAAGACAGAGCTGGTCCCCCGACCCCTTTCCGGCTATGGTAGCAAGAGGATTGGCCCCAAC 300
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Db 342 AAAGACAGAGCTGGTCCCCCTGACCCCTTTTGGCTACGGCAGCAAGAGGATTGGCCCCTAAC 401
QY 301 GGTGATGTGGTGGTTCGAATACCTCTCTCTCAACACCAACCCCTGATGTATCTCACC 360
Db 402 GCGGATGTGGTGGTTCGAATACCTCTCTCTCAACACCAACCCCTGATGTATCTCACC 461
QY 361 AAATCACTTTGCAATTTTCCGAGAAAATCCTCATCTTTTCAGGGCGGTGCTGAGGAACTAC 420
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QY 421 ATTACAGCAGTGAAGAAACATGTGCTATGCGGTGTTGGAATTTGATGCGGAGGGGTTGGGG 480
Db 522 ATTACAGCAGTGAAGAAACATGTGCTATGAGGTGTTGGAATTTGATGCGTCAAGGATTTGGGG 581
QY 481 ATAAGCCAGAGAAATACGTTTAAGCAGGTTGCTGAGGATGAGAAAGTCAATCTGCTCTTC 540
Db 582 ATAAGCCAGAGAAATGTTGTTGAGTGGTTCGAAAGGATGAGAAAGTCAATCTGCTCTTC 641
QY 541 AGGTTGAACCACTTACCCGCTTTGCCCTGAGGTGCAAGCACTGAAC---CGGAATTTGGTT 597
Db 642 AGACTTAACCACTTACCCGCTATGCCGAGGTGCAAGCAATTTGACCGAAGGAATTTGGTT 701
QY 598 GGGTTTGGGAGCACACAGACCCACAGATAAATTTCTGTCTTAAGATCTAACAGCACATCT 657
Db 702 GGAATTTGGAGAGCACACAGACCCACAGATAAATTTCTGTCTTGAGATCTAACAGCACCTCA 761
QY 658 GGCCTGCAAAATCTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCC 717
Db 762 GGCCTGCAAAATCTGTCTCAGATGGCACTTGGGTTTCTGTCCCACTGATCAAACTTCC 821
QY 718 TTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTA 777
Db 822 TTTTTCATCAATGTTGGTGACGCTCTTTCAGGTAATGACTAATGGGAGGTTTAAAAGTGTA 881
QY 778 AAGCATAGGTTTGGCTGACCAACCAAGTCAAGGTTATCAATGATCTACTTTTGAGGA 837
Db 882 AAGCATAGGTTTGGCTGACCAACCAAGTCAAGGTTTCAATGATCTACTTTTGAGGA 941
QY 838 CCAGCGTTCAGTGAAAATATAGCACTTTTACCTTCAGTGTATTAAGAGGAGGAGTCT 897
Db 942 CCAGCGTTCAGTGAAAATATAGCACTTTTACCTTCAGTGTATTAAGAGGAGGAGTCT 1001
QY 898 TTGTACAAAGAGTTTCATGTTGTGTAATAACAAGAGGCTGCGTACACTTCAAGGCTAGCT 957
Db 1002 TTCTACAAAGAGTTTCATGTTGGGTAATACAGAGGCTGCGTACCGCTCAGGCTAGCG 1061
QY 958 GATAATAGGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 996
Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGAT 1100

RESULT 8
AY588978 1406 bp mRNA linear PLN 01-MAY-2005
LOCUS AY588978
DEFINITION Nerium oleander gibberellin 2 oxidase (GA2ox3) mRNA, complete cds.
ACCESSION AY588978
VERSION AY588978.1 GI:50293060
KEYWORDS
SOURCE Nerium oleander (common oleander)
ORGANISM Nerium oleander
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Gentianales; Apocynaceae; Apocynaceae;
Wrighteae; Nerium.
REFERENCE 1 (bases 1 to 1406)
AUTHORS Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
TITLE Isolation, characterization and multi-site polyadenylation of genes
GA 20-oxidases and GA 2-oxidases in Nerium oleander
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1406)
AUTHORS Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
TITLE Direct Submission
```


JOURNAL Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas, CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn, Valencia 46022, Spain

FEATURES
Location/Qualifiers
1..1406
/organism="Nerium oleander"
/mol_type="mRNA"
/db_xref="taxon:63479"
1..1406
/gene="GA2ox3"
1..1005
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/note="GA 2-oxidase; NoGA2ox3"
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ORIGIN
Query Match 48.6%; Score 483.8; DB 15; Length 1406;
Best Local Similarity 71.1%; Pred. No. 2.1e-135;
Matches 669; Conservative 0; Mismatches 266; Indels 6; Gaps 2;
QY 51 ATTCAAGTCCAGCCCTTGTTCACGGGATTTCTGTGTGTCGACCTCACGCCACCCGATGC 110
DB 57 ATTCCCTCCACCAACTTCTACGAAGAAATCTGTGATTGACCTTCTCAAACTCGAGGC 116
QY 111 CAAGATCTCATAGTGAAGCCCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGG 170
DB 117 AAACACTGAATAGTTAAGCCCTGTCAAGAGTTTGAATCTTTAAGGTGATCAATCATGG 176
QY 171 TGTTCATTGGAGTTAATGCCAAATTTAGAAACGAGGCGCTCAGGTTCTTTAAAAAATC 230
DB 177 TGTCTCTTGGAGTTCAATACGAGCTAGAAGTGAAGCTGTCAAGTCTTCTCAATTACC 236
QY 231 TCAGTCCGAGAAAGACAGAGCTGTTCCCGACCCCTTTCCGGGTATGGTAGCAAGAGAT 290
DB 237 CCAACACAGAGAAAGAAAGTTTCGCCCTCTCTAAACCTTTTGGCTATGGTAAACAAGAGAT 296
QY 291 TGGCCCAACCGGTGATGTCGGTGGTTCGAATACCTCTCCTCAACCAACCCGTATGT 350
DB 297 TGGCCAGAACGGGTGATGTGGGTGGATGATGATCTTCTCTTAACCAACCAATCTCGAAT 356
QY 351 TATCTCACCCAAATCACTTTGCAATTTCCGAGAAATCTCATCAATTTCCAGGCGGTGT 410
DB 357 AGTTTACGAGAAAGCGT---CACCATCCCGCGGATTCAGAACCTTTCTGCTTGTGT 413
QY 411 GGAGAACTACATTACAGCAGTAGGAAGAACATGTGCTATGCGGTGTGGAAATGATGCCGA 470
DB 414 GAATGACTATGTTCAGCGGTGAGAAGTATGGCTGTGATGTTCTGGACATGATTGCAGA 473
QY 471 GGGTTGGGGATAAGCAGAGGAATACGTTAGCAGGTTGCTGAAGGATGAGAAAGTGA 530
DB 474 TGGACTGAAGATTTGGGCCAAGGAATGTGCTGAGCAGGCTTTTAAAGAGATGAGAAAGCGA 533
QY 531 TTTCGTGCTTCAGGTGAACCACTACCCGCTTGGCCCTGAGGTGCAAGCACTGAAC---CG 587
DB 534 CGTGTCTTCAGGCTAAACCACTATCCACATGTCCAGAGCTTCAAGCATTTAGTGGTGC 593
QY 588 GAATTTGGTTGGTTGGGAGACACACAGCCACAGATAAATTCGTCTTAAAGATCTAA 647
DB 594 AAATTTGATGGTTCCGAGAACACACAGATCTCTCAATAATATCTGTTGTGAGATCTAA 653
QY 648 CAGCAGATCTGGTTGCAATCTGTCTCACAGATGGCACTTGGGTTTCAATCCACCTGA 707
DB 654 CAACATCAGGCTGCAAAATCTCTCTGAAGAATGGGACATGGGTTTCAATCCCTCTGA 713

QY 708 TCAGACTTCTCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGAGGTT 767
DB 714 TCAGTACTCTCTTTTTCATTAATGTTGGTGATTCCTTGCAGGTAATGACTAATGGAGAT 773
QY 768 TAAAGTCTAAGCATAGGTTTGGCTGACACACGAGTCAAGGTTATCAATGATCTA 827
DB 774 TAGGAGTGTAAAGCATAGAGTTTTCGACGGCTTGAAGTCGAGGGTATCCATGATCTA 833
QY 828 CTTTCGAGGACAGCGTTGAGTGAATAATATAGCACTTTACCTTCAGTGATCTTAAAGG 887
DB 834 CTTAGGAGGACCACTTTGGATGAAGAATAGCCCTTTATCTCACTAATGGAGGAGG 893
QY 888 AGAGGAGTGTGTACAAAGAGTTCACATGGTGTGAATACAAAGAGGTCCTCACATTC 947
DB 894 TGAAGAAAGTTGTATAAGGAATTCACATGGTGTGAATACAAAGAGTCACTTACAAGAC 953
QY 948 AAGGCTACTGATATATAGCTTGCCTTCCAGCAAAATCTG 988
DB 954 GAGGCTTGGTGACACAGGCTCAAAATCTTTGAGAAATCTG 994

RESULT 9
AY594292 1245 bp mRNA linear PLN 30-APR-2005
LOCUS Nerium oleander GA 2-oxidase 2 mRNA, complete cds.
DEFINITION AY594292
ACCESSION AY594292
VERSION AY594292.1 GI:51011365
KEYWORDS
SOURCE Nerium oleander (common oleander)
ORGANISM
Nerium oleander
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Gentianales; Apocynaceae; Apocynaceae; Apocynaceae; Wrightieae; Nerium.
REFERENCE 1 (bases 1 to 1245)
Uboda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Isolation, characterization and multi-site polyadenylation of GA 20-oxidases and GA 2-oxidases in Nerium oleander
Unpublished
2 (bases 1 to 1245)
Uboda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Direct Submission
Submitted (08-APR-2004) Instituto de Biologia Molecular y Celular de Plantas, Consejo Superior de Investigaciones Cientificas (CSIC), Universidad Politecnica de Valencia, Avda. de los Naranjos s/n, Valencia 46022, Spain
FEATURES
Location/Qualifiers
1..1245
/organism="Nerium oleander"
/mol_type="mRNA"
/db_xref="taxon:63479"
1..999
/note="GA2ox2"
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/product="GA 2-oxidase 2"
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ORIGIN
Query Match 46.6%; Score 463.8; DB 15; Length 1245;
Best Local Similarity 68.0%; Pred. No. 2.5e-129;
Matches 677; Conservative 0; Mismatches 312; Indels 6; Gaps 2;
QY 1 ATGGTTGTTCTGCTCAGCAGCATTTGAACCAAGTTTCTTCTTCTGAACCATTCAGTCC 60
DB 1 ATGGTGGTCTTGTGTCANACCAAGCAATGGAACAGTCTCTGCTTAGTCAAGAACTGTAAAGCT 60

QY 61 ACGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCAGCGACCCCGATGCAAGATCTC 120
Db 61 CCACATATTCCGGGTGTTCATGTATAGACTCTCGNAACCTGACTCGAAGACCTC 120
QY 121 ATAGTGAACGCTGTAGGAGCTTCGGCTCTTCAAGCTTGTGAACCATGTTGTTCATTC 180
Db 121 CTGTGTAAGGCTGTCAAGAGTTGGATTTTCAAAGTCATTAATCAAGGTGTTCACACC 180
QY 181 GAGTTAATGGCCOATTTAGAAACGAGGCGCTCAGGTTCTTTAAATAATCTCAGTCCGAG 240
Db 181 GAATTCATCAACCAACTTGAGTCTGAAGCTGTCAAAATTTCTCTTTGGCCCTTTCCGAT 240
QY 241 AAAGACAGAGCTGTCCCCCGACCTTTCCGGCTATGTGTAAGAGGATGGCCCCAAC 300
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QY 301 GGTGATTCGGTTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCC 360
Db 301 GCGATATCGATGGGTGTAATACATCATCTATCAACCAATCCGAATTCMAATTACCAA 360
QY 361 AATCACTTTGCATTTCCGAGAAATCCTCATCTTCAAGGCGGTGGTGGAACTAC 420
Db 361 AGATTTGAATCAATTTTGGCATGACCCCAAGAAAATTTGCGATGCTGTATGACTAC 420
QY 421 ATTACAGCAGTGAAGAACATGCTATGCGGTGTGGAAATGATGGCGAGGGTTGGGG 480
Db 421 GTATCATCAGTAAGAAATATGGCTGTGAATATCTTGAATTAATGCGAGAGGTTGAAT 480
QY 481 ATAAGGACAGGAAATACGTTAAGCAGTTGCTGAAGGATGAGAAAATGATTCGTCCTC 540
Db 481 ATTCAGCCAAAGAAGCTGTTTCAGCAAGCTCTTGATGATGAACAGAGTGACTCTGTTTC 540
QY 541 AGTTGAAACACTACCGGCTTCGCTGAGGTGCAAGCACTGAA---COGGAATTTGGTT 597
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QY 598 GGGTTTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAAACACACATCT 657
Db 601 GGTTTTGGAGAACACATGACCTGACCCACAAATCATCTGTCTTAAGATCAAAACACTTCT 660
QY 658 GGCTTGCAATCTGTCTCAGAGATGGCATTGGGTTTCAGTCCCACTGATCAGACTTC 717
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QY 718 TTTTTCATCAATGTTGTGACGCTCTACAGGTAATGACTAATCGGAGGTTTAAAGTGA 777
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QY 778 AAGCATAGGGTTTTGGCTGACACAAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGA 837
Db 781 AAGCATAGGGTTTTGGCAACAGATATGNAATCCAGGCTTTCGATGATTTATTTGGAGGA 840
QY 838 CCAGCGTTGAGTGAATAATAGACCTTTTACCTTTCAGTGTATGTTAAAGGAGGAGTGT 897
Db 841 CCACCGTTGAGTGAGAAGATAGCTCCATTCCTACCTACTTATG---GAAGGTGAAGACAGC 897
QY 898 TTGTACAAAGAGTTACATGGTGTGAATACAAAGAGCTCGGTACACTTCAAGGCTAGCT 957
Db 898 TTGTACAAAGAGTTACATGGTTGAGTACAAAGAGTCTGCATACAAAGTCAAGTCAAGTACTAGCT 957
QY 958 GATAATAGGCTTGCCCTTTCCAGAAATCTGCTGC 992
Db 958 GATAACAGACTGCTCTGTTTGAGAAATTTGCTGC 992

RESULT 10
CWA315663 1383 bp mRNA linear PLN 19-JUN-2003
LOCUS Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox
DEFINITION gene).
ACCESSION AJ315663
VERSION AJ315663.1 GI:32127336

KEYWORDS

SOURCE

ORGANISM

ga2ox gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)

Cucurbita maxima

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .1383

/organism="Cucurbita maxima"

/mol_type="mRNA"

/cultivar="Riesenmelone, gelb genetzt"

/db_xref="taxon:3661"

/clone="2beta-WS2"

/tissue_type="root tips"

/dev_stage="7 day old seedling"

1. .1383

/gene="ga2ox"

43. .1008

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/product="Gibberellin 2-oxidase"

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ORIGIN

Query Match 46.3%; Score 461.2; DB 15; Length 1383;

Best Local Similarity 69.0%; Pred. No. 1.6e-128;

Matches 647; Conservative 0; Mismatches 288; Indels 3; Gaps 1;

QY 58 TCACGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCAGCACCCCGATGCAAGAT 117

Db 64 TCTGCAGCATTTCTACTCTGGGATTCATTTGATAGACCTCTCTGCACAGATGCTAAACA 123

QY 118 CTCATAGTGAACGCCCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCCA 177

Db 124 CTATTGTCAAGCTTGTGAAGACTCGGATCTTTAAGTTGTCAACATGTTGTCCTCC 183

QY 178 TTGGAGTTAATGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 237

Db 184 ATGGAATTAATCTCTCTCTTGAATCAGAATCCACCAAAATCTCTCTCCCTCTCTCT 243

QY 238 GAGAAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGTTAGCAGAGGATTTGCCCA 297

Db 244 GAAAAACAGAGAGCTGGCCCTCTCTCCCTTTTGGCTATGGAACAAACAAAATTTGCCCGC 303

QY 298 AACGGTGTATCGGTTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTTATCTCA 357

Db 304 AATGGCGATGTGCGTTGGGTGGAATATCTCTTTGAACTCATCTCGAATCCNACTCC 363

QY 358 CCAAAATCACTTTGCAATTTCCGAGAAAATCTCATCATTTCAAGGCGGTGGGGAAC 417

Db 364 GATGGGTTCCTCTCCATTTTCGGCCCAAGACCCACAAAACCTCCGCTCTCTGCTGTAACGAT 423

QY 418 TACATTACAGCAGTGAAGAACATGCTGCTATGCGGTGTTGGAATTTGATGGCGGAGGGTTG 477

Db 424 TACATCTCGGCTGTGAGGAACATTTGGCGGGTGAAATCCTCGAGCTAATTTGGCGGAAGGGTTG 483

QY 478 GGGATAGCGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGC 537
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Db 484 AAGATTCAACACGAAACGTTTCAGTAGCTCGTGATGATGAACAGAGGACTCTGTT 543
QY 538 TTCAGGTTGAACCACTACCGCTTCCCTGAGGTGCAAGCACTGAACCG---GAATTG 594
Db 544 TTCAGAGTGAACCAATATCCGCGCATGTCAGAACCTTCAAGCTTTAAAGAGAAACAACATG 603
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Db 604 ATTGGATTGGAGAACACAGACCCCTCAATCATTTTCAGTTTGGATCAACAACACT 663
QY 655 TCTGGCTTCAAAATCTCTCAGATGCACTTGGGTTTCAGTCCCACTGATCAGACT 714
Db 664 TCTGGATTCAAAATCTCTCGCAGATGGAATGGATATCTGTTCTCCCGATCACAGC 723
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Db 784 GTGAAGCATAGGTTTGGTCAACAGCTCAAGTCAAGGTTTCAATGATCTACTTCGT 843
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Db 844 GGGCCACCGTTGAGTGAAGATAGCTCTCTTAGCTTCCCTTATGCAAGGAGAAAGA 903
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Db 964 GCTGACAAAGCTTGTGCCCTTTGAAAGATTGCAGC 1001

RESULT 11

CMA302041 1308 bp mRNA linear PLN 16-DEC-2002
LOCUS Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene).
DEFINITION AJ302041
VERSION AJ302041.1 GI:27123664
KEYWORDS ga2ox gene; gibberellin 2-oxidase.
SOURCE Cucurbita maxima (winter squash)
ORGANISM Cucurbita maxima

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.

REFERENCE

1 Friese, A. and Lange, T.

Expression studies on the major Gibberellin dioxygenases in

developing seeds of Cucurbita maxima L

Unpublished

2 (bases 1 to 1308)

Lange, T.

Direct Submission

Submitted (14-DEC-2000) Lange T., Botanical Institute, Dept. Plant

Physiology and Biochemistry, TU Braunschweig, Mendelssohnstr. 4,

Braunschweig, D-38106, GERMANY

Location/Qualifiers

1. .1308

/organism="Cucurbita maxima"

/mol_type="mRNA"

/cultivar="Riesenmelone, gelb genetzt"

/db_xref="taxon:3661"

/clone="2beta-EMBRYO"

/dev_stage="developing embryos"

1. .1308

/gene="ga2ox"

87. .1052

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gene

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/product="gibberellin 2-oxidase"

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/translation="MAAASFSAFYGIPLDLSAPDAKQLIVKACBELGFFKVKH

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DEQSDSVRVNHYPCPLQALKNTNMGFGEHTDPOIISVLRSNNTSGFOJSLADGN

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ORIGIN

Query Match 46.0%; Score 458; DB 15; Length 1308;
Best Local Similarity 68.8%; Pred. No. 1.5e-127;
Matches 645; Conservative 0; Mismatches 290; Indels 3; Gaps 1;
QY 58 TCCAGCCCTTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGCACCCCGATGCCAAGAT 117
Db 108 TCTGCAGCATTTCTACTCTGGGATTCATTTGATGACCTCTCTGCACAGATCTAAACAA 167
QY 118 CTCATAGTGAACGCTGTAGGACTTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCCA 177
Db 168 CTCATTGTCAAAAGCTTGTGAAGAACTCGGATTTCTTTAAAGTTGTCAAAACATGTTG 227
QY 178 TTGGAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 237
Db 228 ATGGAATTAATCTCTCTCTTGAATCAGAATCCACCAATTTCTTCCCTTCCCTCTCT 287
QY 238 GAGAAAGCAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTGAGCAAGAGGATTTGGCCCA 297
Db 288 GAAAACAGAGAGCTGGCCCTCTTCCCTTTTGGCTATGGAACAACAACATTTGGCCGC 347
QY 298 AACGTGATGTCGGTTGGGTGGAATACCTCTCTCTCAACCAACCACTGATGTTATCTCA 357
Db 348 AATGGCATGTGCGTTGGGTTGAATATCTCTCTTTGAACACTCATCTCGAATCCAACTCG 407
QY 358 CCCAAATCACCTTTCATTTCCGAGAAAATCCTCATCATTTTCAGGGCGGTGGAGAAC 417
Db 408 GATGGGTTTCTCTCCATTTTGGCCAGACCCACAAAACACTCCGCTCTCTGTGAACGAT 467
QY 418 TACATTACAGCAGTCAAGAACATGTGCTATGCGGTGTTTGGAAATGATGCGGAGGGGTTG 477
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QY 478 GGGATAAGCGCAGAGAAATACGTTAAGAGAGTTGCTGAAGGATGAGAAAAGTGAATCGTGC 537
Db 528 AAGATTCAACAAACGAAACGTTTTCAGTAAGCTCGTGATGATGAACAGAGCGACTCTGTT 587
QY 538 TTCAGGTTGAACCACTACCGCTTCCCTGAGGTGCAAGCACTCAACCG---GAATTG 594
Db 588 TTCAGAGTGAACCATTTATCCGCCATGTCCAGACCTTCAAGCTTTAAAGAGAAACAACATG 647
QY 595 GTTGGGTTTGGGGAGCAGACAGACCCACAGATAATTTCTGTCTTAAAGATCTTAACAGCACA 654
Db 648 ATTGGAATTTGGAGAACACAGACCCCTCAATCATTTTCAGTTTGGATCAACAACACT 707
QY 655 TCTGCTTGCAAAATCTGCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACT 714
Db 708 TCTGGATTTCAAAATCTCTCTCGCAGATGGAATTTGATATCTGTTCTCCCGATCACAGC 767
QY 715 TCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGT 774
Db 768 TCTCTTCTTCATCAATGTTGGTGACTCTTTACAGGTGATGACTAATGGAAGATTTCAAAAGT 827
QY 775 GTAAAGCATAGGTTTTCGTCGACACAACGAAGTCAAGGTATCAATGATCTACTTTTGA 834
Db 828 GTGAAGCATAGGTTTTCACAAACAGCTCGAAGTCAAGGTTTCAATGATCTACTTCGCT 887
QY 835 GGACCAGCGTTGAGTGAATAATATAGCACCTTTTACCTTCAGTGAATGTTAAAGAGAGGAG 894

Db	888	GGGCCACCGTTGAGTGAAGAGATAGCTCCCTTTAGCTTCCTTATGCAAGGAGAAAGA	947
Qy	895	TGTTTGTACAAAGAGTTTCACATGCTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTA	954
Db	948	AGTTTGTACAAAGAGTTTACATGTTTGTAGTACAAAGATCAGTTTACAACTCCAGTTG	1007
Qy	955	GCTGATATAGGCTGTCGCCCTTTCCAGAAATCTGCTGC	992
Db	1008	GCTGACAAACAGGCTGTGCGCCTTTGAAAGAAATTCGACG	1045
RESULT 12			
AB125232			
LOCUS			
DEFINITION	AB125232	1292 bp mRNA linear	PLN 29-APR-2004
	Nicotiana tabacum GA2ox1 mRNA for gibberellin 2-oxidase 1, complete cds.		
ACCESSION	AB125232		
VERSION	AB125232.1	GI:46849528	
KEYWORDS			
SOURCE			
ORGANISM			
	Nicotiana tabacum (common tobacco)		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
gene			
CDS			
ORIGIN			
Query Match		44.5%	Score 443; DB 15; Length 1292;
Best Local Similarity		66.7%	Pred. No. 5.5e-123;
Matches	664; Conservative	0; Mismatches 325; Indels 6; Gaps 2;	
Qy	1	ATGGTGTCTCTGCTCAGCCAGCATTTGAACCGAGTTTTTCCCTTCTGTGAACCAATTCAGATCC	60
Db	75	ATGGTGTCTTAACTAAACCTGGCAATTCAGCAATTTCCCACTAGTCAAAAACTGCAAAATTA	134
Qy	61	ACGCCCTTGTTCACGGGGATTTCCTGTCGTCGACCTCAGCACCCGATGCCAAGAATCTC	120
Db	135	TCCTCATTTCTCAATGTGTTCATGATAGACCTCTCTAACTAATCTTAAGACCTT	194
Qy	121	ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCAATGGTGTTCATTTG	180

Search completed: December 27, 2005, 21:42:44
Job time : 5303.67 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 16:12:28 ; Search time 671.461 Seconds
(without alignments)
9885.961 Million cell updates/sec

Title: US-10-670-454-1_COPY_68_1063

Perfect score: 996

Sequence: 1 atggtgtctgtctcagcc.....tcagaaatctgtcgtgat 996

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	100.0	999	13	ADT62692
2	996	100.0	1318	3	AAZ55912
3	827.4	83.1	1359	3	AAZ99471
4	827.4	83.1	1359	6	AAZ99471 Soybean g
5	424.4	42.6	1026	6	AD40261
6	424.4	42.6	1026	6	AB213545
7	424.4	42.6	1026	8	AD467975
8	421.4	42.3	1352	12	AAZ55916
9	421.4	42.3	1352	12	AD40261 Arabidops
10	418.2	42.0	1403	3	AAZ99472
11	418.2	42.0	1403	6	AAZ99472 Soybean g
12	381.6	38.3	1008	3	AAZ55917
13	362.6	36.4	1473	12	AD40261 Arabidops
14	356.6	35.8	1224	3	AAZ99472
15	356.6	35.8	1316	3	AAZ55915
16	355.6	35.7	1651	14	AB213545
17	354	35.5	984	8	AD40261
18	354	35.5	984	12	AD40261
19	354	35.5	1271	14	AB213545

20	354	35.5	1650	12	ADM94203
21	314.2	31.5	1555	12	ADM94201
22	307.8	30.9	783	3	AAZ99474
23	307.8	30.9	783	6	AAZ99474 Cotton g1
24	301.6	30.3	831	13	AD40261
25	285	28.6	927	12	AD40261
26	272.6	27.4	860	13	AD40261
27	188.6	18.9	1322	13	AD40261
28	187	18.8	1065	8	AD40261
29	172.2	17.3	919	13	AD40261
30	166	16.7	811	3	AAZ99478
31	166	16.7	811	6	AAZ99478 Maize gib
32	161.8	16.2	95769	8	AAZ99478 Maize gib
33	156.2	15.7	504	12	AD40261
34	155.6	15.6	403	3	AAZ99473
35	155.6	15.6	403	6	AAZ99473 Soybean g
36	154.8	15.5	406	3	AAZ99475
37	154.8	15.5	406	6	AAZ99475 Cotton g1
38	152.4	15.3	966	3	AAZ99469
39	152.4	15.3	966	6	AAZ99469 Arabidops
40	150.4	15.1	537	12	AD40261
41	141	14.2	480	3	AAZ50271
42	132	13.3	683	3	AAZ50271 Arabidops
43	130.4	13.1	687	3	AAZ50271
44	120	12.0	426	3	AAZ50271
45	120	12.0	426	6	AAZ50271

ALIGNMENTS

RESULT 1

ADT62692
ID ADT62692 standard; DNA; 999 BP.

XX
AC ADT62692;

XX
DT 13-JAN-2005 (first entry)

XX
DE DNA encoding Phaseolus coccineus gibberellin 2-oxidase.

XX
KW DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene;
expression cassette; transgenic plant; transgenic; plant;
gibberellin 2-oxidase; ds.

XX
OS Phaseolus coccineus.

XX
PN WO2004092390-A2.

XX
PD 28-OCT-2004.

XX
PF 09-APR-2004; 2004WO-US011000.

XX
PR 09-APR-2003; 2003US-0461459P.

XX
PM (MONS) MONSANTO TECHNOLOGY LLC.

XX
PI Gilbertson L, Krieger E, Zhang W, Ye X;

XX
DR WPI; 2004-758349/74.

XX
PT New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid

PT first border region linked to a transgene linked to an Agrobacterium Ti
plasmid second border region, useful for enhancing production of
transgenic plants.

XX
PS Example 1; SEQ ID NO 3; 77pp; English.

XX
CC The present invention relates to a DNA plasmid comprising a transfer DNA
(T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
to at least one transgene linked to an Agrobacterium Ti plasmid second
border region, and located in the DNA plasmid outside of the T-DNA is a
plant expression cassette comprising a plant cell non-lethal negative

selectable marker gene linked to a vector backbone DNA. Also disclosed are a method for enhancing the selection of transgenic plants that do not contain vector backbone DNA, a method for reducing the copy number of a transgene in a plant cell, and a transgenic plant produced by the method. The DNA plasmid comprises the expression cassette comprising a promoter that functions in plant cells operably linked to a plant cell non-lethal negative selection marker gene. The promoter is a constitutive promoter. The promoter expresses the linked non-lethal negative selection marker gene product in tissue culture during plant regeneration. The plant cell non-lethal negative selectable marker gene comprises a plant hormone biosynthetic pathway gene, degradative gene, biosynthetic pathway substrate-diverting gene or signalling gene, or metabolic interference gene. The transgene is a plant positive selectable marker gene selected from antibiotic resistance and herbicide resistance. The transgene comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway gene is selected from gibberellin acid pathway genes, cytokinin pathway genes, auxin pathway genes, ethylene pathway genes, and abscisic acid pathway genes. The plasmid is useful for enhancing the production of commercially viable transgenic plants. The present sequence represents DNA encoding phaseolus coccineus gibberellin 2-oxidase. The sequence is used as a non-lethal negative selectable marker gene.

XX SQ Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

Query Match 100.0%; Score 996; DB 13; Length 999;
Best Local Similarity 100.0%; Pred. No. 5.8e-310; Indels 0; Gaps 0;
Matches 996; Conservative 0; Mismatches 0;

QY 1 ATGTTGTTCTGTCTCAGCGAGCATTTGAACACAGTTTTCCTTCTGAAACCATTCAGTCC 60
DB 1 ATGTTGTTCTGTCTCAGCGAGCATTTGAACACAGTTTTCCTTCTGAAACCATTCAGTCC 60

QY 61 AGCCCTTGTTCACGGGGATTCCTGTGTGTCAGCTCAGCGACCCCGATGCCAAGATCTC 120
DB 61 AGCCCTTGTTCACGGGGATTCCTGTGTGTCAGCTCAGCGACCCCGATGCCAAGATCTC 120

QY 121 ATAGTCAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTGTCCATTG 180
DB 121 ATAGTCAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTGTCCATTG 180

QY 181 GAGTTAATGGCCAAATTTAGAAACGAGGCGCTCAGGTTCCTTTAAATAATCTCAGTCCGAG 240
DB 181 GAGTTAATGGCCAAATTTAGAAACGAGGCGCTCAGGTTCCTTTAAATAATCTCAGTCCGAG 240

QY 241 AAAGACAGAGCTGGTCCCCCGACCTTCGGCTATGTGATGACAGAGGATTCGCCCAAC 300
DB 241 AAAGACAGAGCTGGTCCCCCGACCTTCGGCTATGTGATGACAGAGGATTCGCCCAAC 300

QY 301 GGTGATGTCGGTGGTTCGAATACCTTCCTCAACACCAACCTCATGTATCTCACCC 360
DB 301 GGTGATGTCGGTGGTTCGAATACCTTCCTCAACACCAACCTCATGTATCTCACCC 360

QY 361 AAATCACTTTGCAATTTCCGAGAAATCCTCATCTTTTCAGGCGGTGTGAGAACTAC 420
DB 361 AAATCACTTTGCAATTTCCGAGAAATCCTCATCTTTTCAGGCGGTGTGAGAACTAC 420

QY 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAATTTGATGCGGAGGGTTGGGG 480
DB 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAATTTGATGCGGAGGGTTGGGG 480

QY 481 ATAAGGACAGGAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAGTGTGTCGTCCTC 540
DB 481 ATAAGGACAGGAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAGTGTGTCGTCCTC 540

QY 541 AGGTTGAACCACTACCGCCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGG 600
DB 541 AGGTTGAACCACTACCGCCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGG 600

QY 601 TTTGGGAGCAGACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGGC 660
DB 601 TTTGGGAGCAGACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGGC 660

QY 661 TTGCAAACTGTCTCAGATGGCAGTGGGTTTCAGTCCACCTCATCAGACTTCCTTT 720
DB 661 TTGCAAACTGTCTCAGATGGCAGTGGGTTTCAGTCCACCTCATCAGACTTCCTTT 720

QY 721 TTCATCAATGTTGGTGAGCGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAG 780
DB 721 TTCATCAATGTTGGTGAGCGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAG 780

QY 781 CATAGGGTTTGGCTGCACACAGCAAGTCAAGGTTTATCAATGATCTACTTTCGAGGACCA 840
DB 781 CATAGGGTTTGGCTGCACACAGCAAGTCAAGGTTTATCAATGATCTACTTTCGAGGACCA 840

QY 841 GCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGTATTTAAAAGGAGAGGAGTGTG 900
DB 841 GCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGTATTTAAAAGGAGAGGAGTGTG 900

QY 901 TACAAAGAGTTCACATGTTGTAATACAAAGAGGTCGCTACACTTCAAGGCTAGCTGAT 960
DB 901 TACAAAGAGTTCACATGTTGTAATACAAAGAGGTCGCTACACTTCAAGGCTAGCTGAT 960

QY 961 AATAGGCTTGGCCCTTCCAGAAATCTGCTGCTGAT 996
DB 961 AATAGGCTTGGCCCTTCCAGAAATCTGCTGCTGAT 996

RESULT 2
AAZ55912 ID AAZ55912 standard; cDNA; 1318 BP.
XX AC AAZ55912;
XX AC AAZ55912;
DT 10-APR-2000 (first entry)
XX DE Runner bean gibberellin 2-oxidase PcGA2ox1 cDNA.
XX DE Runner bean gibberellin 2-oxidase PcGA2ox1 cDNA.
KW Gibberellin 2-oxidase; PcGA2ox1; runner bean; 2-beta-hydroxylation;
KW inactivation; growth inhibition; ss.
XX OS Phaseolus coccineus.
XX XX
FH Key Location/Qualifiers
FT CDS 68..1066
FT /*tag= a
FT /product= "Gibberellin 2-oxidase PcGA2ox1"
FT /transl_except= {pos:1058..1063, aa:Ala}
XX
PN WO9966029-A2.
XX
PD 23-DEC-1999.
XX
PF 11-JUN-1999; 99WO-GB001857.
XX
PR 12-JUN-1998; 98GB-00012821.
PR 15-JUL-1998; 98GB-00015404.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Thomas SG, Hedden P, Phillips AL;
XX
DR WPI; 2000-097742/08.
DR P-PSDB; AAY58597.
XX
PT New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
PT
PS Claim 1; Fig 1; 42pp; English.
XX
XX This sequence represents cDNA encoding a runner bean gibberellin (GA) 2-oxidase, PcGA2ox1. This enzyme is a GA 2-beta-hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in

CC plants, ensuring that the active hormones do not accumulate in plant
CC tissues. The nucleic acids can be used to transform plants so that
CC gibberellin 2-oxidase can be constitutively over-expressed or otherwise
CC enhanced to reduce the concentration of bioactive GAs in the plants and
CC therefore to inhibit plant growth. Growth inhibition is useful in many
CC agricultural and horticultural applications such as enhancing lodging-
CC resistance and grain yield in cereals, improving seedling quality,
CC reducing the growth of amenity grasses, reducing shoot growth in orchard
CC and ornamental trees, improving tolerance to cold, drought and infection,
CC and increasing yields (by the diversion of assimilates from vegetative to
CC reproductive organs). The nucleic acids may also be used to induce male
CC and/or female sterility (by expression in floral organs), prevent pre-
CC harvest sprouting, reduce shoot growth in hedging plants, inhibit
CC reversibility in the development or germination of seeds and reduce shoot
CC growth in commercial wood species. Antisense constructs of the nucleic
CC acids can also be used to transform plants to reduce the expression of GA
CC 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set
CC and growth in seedless grapes, citrus fruits and pears), improve skin
CC texture and fruit shape in apples, increase stem length and therefore
CC yield in sugar cane, increase yield and earliness in celery and rhubarb,
CC improve malting yields and quality in cereals (particularly barley), and
CC increase growth in woody species

XX
SQ Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;

Query Match 100.0%; Score 996; DB 3; Length 1318;
Best Local Similarity 100.0%; Pred. No. 6.7e-310;
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTCTCTCAGCCAGCATGAACAGATTTTCCTCTGAAACCAATTCAGTCC 60
DB |||||||
QY 68 ATGGTGTCTCTCAGCCAGCATGAACAGATTTTCCTCTGAAACCAATTCAGTCC 127
DB |||||||
QY 61 AGCCCTTGTTCAAGGGATTCCTGTGGTGCACCTCAGCACCCCGATGCCAAGATCTC 120
DB |||||||
QY 128 AGCCCTTGTTCAAGGGATTCCTGTGGTGCACCTCAGCACCCCGATGCCAAGATCTC 187
DB |||||||
QY 121 ATAGTGAACGCTGTAGGAGCTTCGGCTCTTCAAGCTTGTGAACCATGGTTCATTTG 180
DB |||||||
QY 188 ATAGTGAACGCTGTAGGAGCTTCGGCTCTTCAAGCTTGTGAACCATGGTTCATTTG 247
DB |||||||
QY 181 GAGTTAATGGCCCAATTAGAAGACGAGCCCTCAGGTCTTTAAAAATCTCAGTCCGAG 240
DB |||||||
QY 248 GAGTTAATGGCCCAATTAGAAGACGAGCCCTCAGGTCTTTAAAAATCTCAGTCCGAG 307
DB |||||||
QY 241 AAAGACAGAGCTGTGTCCTCCCGACCTTTCGGCTATGTTAGCAGAGATTGCGCCAAAC 300
DB |||||||
QY 308 AAAGACAGAGCTGTGTCCTCCCGACCTTTCGGCTATGTTAGCAGAGATTGCGCCAAAC 367
DB |||||||
QY 301 GGTGATGTGGGTGGATGCAATACCTCTCTCAACACCAACCTGTATCTCAACC 360
DB |||||||
QY 368 GGTGATGTGGGTGGATGCAATACCTCTCTCAACACCAACCTGTATCTCAACC 427
DB |||||||
QY 361 AAATCACTTTGATTTTCGAGAAAATCTCATATTTTCAGGCGGTGGTGGAGAACTAC 420
DB |||||||
QY 428 AAATCACTTTGATTTTCGAGAAAATCTCATATTTTCAGGCGGTGGTGGAGAACTAC 487
DB |||||||
QY 421 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAATTCATGCGGAGGGTTGGG 480
DB |||||||
QY 488 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAATTCATGCGGAGGGTTGGG 547
DB |||||||
QY 481 ATAAGCGAGAGGAATACGTTTAAGCAGGTTGCTGAAAGGATGAGAAAAGTATTCGTGCTTC 540
DB |||||||
QY 548 ATAAGCGAGAGGAATACGTTTAAGCAGGTTGCTGAAAGGATGAGAAAAGTATTCGTGCTTC 607
DB |||||||
QY 541 AGGTTGAACCACTACCGGCTTTCGCTGAGGTGCGAGCACTGAACCGGAATTTGGTGGG 600
DB |||||||
QY 608 AGGTTGAACCACTACCGGCTTTCGCTGAGGTGCGAGCACTGAACCGGAATTTGGTGGG 667
DB |||||||
QY 601 TTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGACATCTGCG 660
DB |||||||
QY 668 TTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGACATCTGCG 727
DB |||||||

QY 661 TTGCAAAATCTGTCTCAGACAGATGGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTT 720
DB |||||||
QY 728 TTGCAAAATCTGTCTCAGACAGATGGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTT 787
DB |||||||
QY 721 TTTCATCAATGTTGGTGAGCGCTCTACAGGTAATGACTAATGGAGGCTTTAAAAAGTGTAAAG 780
DB |||||||
QY 788 TTTCATCAATGTTGGTGAGCGCTCTACAGGTAATGACTAATGGAGGCTTTAAAAAGTGTAAAG 847
DB |||||||
QY 781 CATAGGGTGTGGTGTGACACAAACGAAGTCAAGGTTTATCAATGATCTACTTTGGAGGACCA 840
DB |||||||
QY 848 CATAGGGTGTGGTGTGACACAAACGAAGTCAAGGTTTATCAATGATCTACTTTGGAGGACCA 907
DB |||||||
QY 841 GCGTTGAGTGAATAATATAGCACCTTTACTCTCAGTGAATGTTAAAAAGAGAGAGTGTG 900
DB |||||||
QY 908 GCGTTGAGTGAATAATATAGCACCTTTACTCTCAGTGAATGTTAAAAAGAGAGAGTGTG 967
DB |||||||
QY 901 TACAAAGAGTTTCACATGCTGTGAAATACAAAGAGGCTGCTACACTTCAAGGCTAGCTGAT 960
DB |||||||
QY 968 TACAAAGAGTTTCACATGCTGTGAAATACAAAGAGGCTGCTACACTTCAAGGCTAGCTGAT 1027
DB |||||||
QY 961 AATAGGCTTGCCCTTTTCCAGAAATCTGCTGCTGAT 996
DB |||||||
QY 1028 AATAGGCTTGCCCTTTTCCAGAAATCTGCTGCTGAT 1063
DB |||||||
RESULT 3
AAZ99471
ID AAZ99471 standard; cDNA; 1359 BP.
XX
AC AAZ99471;
XX
DT 03-JUL-2000 (first entry)
XX
DE Soybean gibberellic acid 2-oxidase 1 cDNA sequence.
XX
KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW seed germination; seedling growth; gibberellin biosynthetic pathway;
KW transgenic plant; hypocotyl; epicotyl; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 102..1103
FT /*tag= a
FT /product= "gibberellic acid 2-oxidase 1"
FT /trans except= (pos: 633..635, aa: Xaa)
FT /note= "Xaa is an unspecified amino acid"
XX
PN WO200009722-A2.
XX
PD 24-FEB-2000.
XX
PF 10-AUG-1999; 99WO-US018066.
XX
PR 10-AUG-1998; 98US-0096111P.
PR 07-JUN-1999; 99US-0137977P.
XX
PA (MONS) MONSANTO CO.
XX
PI Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
PI Piller KJ, Rao S, Ream JE;
XX
XX
DR WPI; 2000-224351/19.
DR P-FSDB; AAY84099.
XX
PT Obtaining transgenic plant useful for controlling seed germination and
PT seedling growth comprises transgene comprising a sequence expressing
PT altered levels of an essential hormone.
XX
PS Claim 45; Page 248; 267pp; English.
XX
CC The present sequence encodes a gibberellic acid 2-oxidase 1 protein

CC etc., and is also useful in storage and transport of seeds to reduce
CC premature germination which may affect agronomic or food quality of the
CC seeds. The present sequence is soybean GA 2-oxidase 1 cDNA
XX
SQ Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;

Query Match 83.1%; Score 827.4; DB 6; Length 1359;
Best Local Similarity 89.9%; Pred. No. 1.7e-255;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;
QY 1 ATGGTTGTTCTCTCTCAGCAGCATTGAACCAAGTTTCTCTCTGAAACCAATTCAAGTCC 60
DB |||||
QY 102 ATGGTTGTTCTCTCAGCAGCATTGAACCAAGTTTCTCTCTGAAACCAATTCAAGTCC 161
DB |||||
QY 61 ACGCCCTGTTTCAACGGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAAGAAATCTC 120
DB |||||
QY 162 ACGCCCTGTTTCAACGGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAAGACCCAC 221
DB |||||
QY 121 ATAGTGAACGCTGTAGGAGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTTTCATG 180
DB |||||
QY 222 ATAGTCAATGCTGAGGAGACTTCGGCTTCTTCAAGCTGCTGAACCCAGCTGTTCCGTTA 281
DB |||||
QY 181 GAGTTAAATGGCCCAATTTAGAAAACGAGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAG 240
DB |||||
QY 282 CAGTTCAATGGCCCAATTTGAAAACGAAACCCCTCGGGTTCTTCAAAAAACCTCAATCCGAG 341
DB |||||
QY 241 AAAGACAGAGCTGCTGCCCGACCCCTTTCGGCTATGTAGTGAAGAGGATTCGCCCAAC 300
DB |||||
QY 342 AAAGACAGAGCTGCTGCCCGACCCCTTTCGGCTATGTAGTGAAGAGGATTCGCCCAAC 401
DB |||||
QY 301 GGTGATGTCGGTGGTTCGAATACCTCTCTTCAACCAACCCCTGATTTATCTCAACC 360
DB |||||
QY 402 GCGGATGTCGGTGGTTCGAATACCTCTCTTCAACCAACCCCTGATTTATCTCAACC 461
DB |||||
QY 361 AATACATCTTTCGATTTTCGAGAAATCTCTCATCTTTCAGGCGGTGTCGAGAACTAC 420
DB |||||
QY 462 AAGTCAAGTTCATTTTCGAGAAATCTCTCATCTTTCAGGCGGTGTCGAGAACTAC 521
DB |||||
QY 421 AATACAGCAGTGAAGAACTATGCTATGCGGTGTTGGAATGATGCGGAGGGTTGGGG 480
DB |||||
QY 522 AATAGAGCGGTGAAGAACTATGCTATGAGGTGTTGGAATGATGCTGAGGGATGGGG 581
DB |||||
QY 481 ATAAGCAGAGAAATACGTTAAGCAGGTGCTGAAGGATGAGAAAGTATTCGTCTTC 540
DB |||||
QY 582 ATAAGCAGAGAAATACGTTAAGCAGGTGCTGAAGGATGAGAAAGTATTCGTCTTC 641
DB |||||
QY 541 AGTTGAACTACCTACCGCTTCCCTGAGGTGTCAGCACTGAAC---CGGAATTTGTT 597
DB |||||
QY 642 AGACTTAACCTACCTACCGCTTCCCTGAGGTGTCAGCACTGAAC---CGGAATTTGTT 701
DB |||||
QY 598 GGGTTGGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTTAACAGCACATCT 657
DB |||||
QY 702 GAATTTGGAGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTTAACAGCACATCT 761
DB |||||
QY 658 GGCCTGCAAAATCTGCTCAAGATGCACTTGGGTTTCAGTCCCACTGATCAGACTTCC 717
DB |||||
QY 762 GGCCTGCAAAATCTGCTCAAGATGCACTTGGGTTTCAGTCCCACTGATCAAACTTCC 821
DB |||||
QY 718 TTTTTCATCAATGTTGGTGAAGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGA 777
DB |||||
QY 822 TTTTTCATCAATGTTGGTGAAGCTCTCTTCAAGGTAATGACTAATGGGAGGTTTAAAGTGA 881
DB |||||
QY 778 AAGCATAGGTTTGGCTGACACCAAGAGTCAAGGTATCAATGATCTACTTTCGAGGA 837
DB |||||
QY 882 AAGCATAGGTTTGGCTGACACCAAGAGTCAAGGTATCAATGATCTACTTTCGAGGA 941
DB |||||
QY 838 CCAGCGTTCAGTCAAAATATAGCACTTTACCTTCAGTATGTTTAAAGGAGAGAGTGT 897
DB |||||
QY 942 CCAGCGTTCAGTCAAAATATAGCACTTTACCTTCAGTATGTTTAAAGGAGAGAGTGT 1001
DB |||||
QY 898 TTGTACAAAGAGTTTCAATGTTGGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCT 957
DB |||||
QY 1002 TTCTACAAAGAGTTTCAATGTTGGTGAATACAGAGGCTGCGTACCGTCAAGGCTAGCG 1061
DB |||||

QY 958 GATAATAGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 996
DB |||||
QY 1062 GATAATAGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 1100
DB |||||

RESULT 5
ABZ13545
ID ABZ13545 standard; DNA; 1026 BP.
XX
AC ABZ13545;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1350.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
XX
PR 26-JAN-2001; 2001US-0264647P.
XX
PR 22-JUN-2001; 2001US-0300111P.
XX
XX (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
XX WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 1350; 577pp + Sequence Listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising: (a) contacting nucleic acid
representative of expressed polynucleotides in the plant cell with an
array or probes representative of the plant cell genome; and (b)
detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the
production of transgenic plants, cells and seeds and in producing plants
with increased tolerance to abiotic stress. The present sequence is that
of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
in methods of the invention. Note: The sequence data for this patent is
not represented in the printed specification but is based on sequence
information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;

Query Match 42.6%; Score 424.4; DB 6; Length 1026;
Best Local Similarity 67.5%; Pred. No. 1.5e-125;
Matches 612; Conservative 0; Mismatches 291; Indels 3; Gaps 1;
QY 79 ATTCCTGTGGTGCAGCTCAGCACCCCGATGCCAAGAAATCTCATAGTGAACCCCTGTAGG 138
DB |||||
QY 91 ATCCCGTCTGCAACTAGCCGATCCGGAAGCGAAACCCGAATCGTAAAGCTGCGAG 150
DB |||||
QY 139 GACTTCGGCTTCTCAAGCTTGTGAACCATGTTGTTCCATTTGAGTGAATGATGCCAATTTA 198
DB |||||
QY 151 GAGTTTCGGGTTCTTCAAGTTCGTAACCAACCGAGTCCGACCCGAACTCATGACTCGGTTA 210
DB |||||
QY 199 GAAACAGAGGCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGTGCC 258
DB |||||
QY 211 GAGCAGGAGGCTATTGGCTTCTTCGGGTTGCTCTTTAAAAAACCGGCCGCTGCCA 270
DB |||||

679	Qy	GATGGCATTGGGTTTCAGTCCCACTGATCAGACATCTCTTTTTCATCAATGTTGGTGAC	738
688	Db	GATGGAAATTGGGTCGCTCCCTCCTGATCACTCTTCTTTCTTAATAATGTTGGAGAT	747
739	Qy	GCTCTACAGGTAACTGACTAAATGGGAGGTTTAAAAGTGTAAGCATAGGGTTTTGGCTGAC	798
748	Db	GCTCTTTCAGGTTATGACTAAACGGGAGGTTCAAGAGTGTTAAACACACAGGGTCTTAGGCCGAT	807
799	Qy	ACAACCAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCAGCGTTGTAGCTGAAATAATA	858
808	Db	ACAAGGAGATCGAGGANTTCAATGATATATTTCCGCGGACCGCCATTGACCGAAGATC	867
859	Qy	GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTCTTTGTACAAAGAGTTTCACATGG	918
868	Db	GCACCATTCGCATGCCTTGTCCCTGAGCAAGATGATGGCTTTTACAAAGAAATTCACATTGG	927
919	Qy	TGTGAATACAAGAAGCGTCGCTACACTTCAAGGCTAGCTGATATAATAGGCTTGCCCCCTTC	978
928	Db	TCTCAATACAAACTTCTGCTTACAAGCTTAAGCTTTGGTGATATAGACTTTGGTCTCTTT	987
979	Qy	CAGAAA	984
988	Db	GAGAAA	993

RESULT 7
AAZ55916
ID AAZ55916 standard; cDNA; 1237 BP.
XX
XX AAZ55916;
XX
XX 10-APR-2000 (first entry)
XX
XX Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA.
XX
XX Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
KW growth inhibition; ss.

OS	Arabidopsis thaliana.	
XX		
XX		
FF	Key	Location/Qualifiers
FT	CDS	109..1134
FT		/tag= a
FT		/product= "Gibberellin 2-oxidase AtGA2ox2"
XX		
XX		
PN	WO9966029-A2.	
XX		
XX		
PD	23-DEC-1999.	

11-JUN-1999; 99WO-GB001857.
XX
12-JUN-1998; 98GB-00012821.
PR
15-JUL-1998; 98GB-00015404.
PR
XX
(UYBR-) UNIV BRISTOL.
PA

XX Thomas SG, Hedden P, Phillips AL;
XX
XX WPI; 2000-097742/08.
DR P-PSDB; AAY58599.
XX
XX New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
PT to produce transgenic plants with improved or altered growth
PT characteristics.

PS Example 3; Fig 7; 42pp; English.

accumulate in plant tissues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed or otherwise enhanced to reduce the concentration of bioactive GAS in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), prevent pre-harvest sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species

Sequence 1237 BP; 356 A; 277 C; 280 G; 324 T; 0 U; 0 Other;

Query Match	42.68;	Score	424.4;	DB	3;	Length	1237;
Best Local Similarity	67.58;	Pred. No.	1.6e-125;				
Matches	612;	Conservative	0;	Mismatches	291;	Indels	3; Gaps
Qy	79	ATTCTGTGTCACACTCAGCACCCCGATGCCAAGAATCTCATAGTGAACGCCTGTAGG	138				
Db	199	ATCCCCGTCCTCAACTAGCCGATCCGGNAGCGRAAACCCGAAATCGTAAGAACCCTGCGAG	258				
Qy	139	GACTTGCGCTTCCTCAAGCTTTGGAACAATGGTGTTCATTTGGAGTTAATGGCCAATTATA	198				
Db	259	GAGTTCCGGTTCCTCAAGGTCGTAACCAACGAGTCGACCCGAACTCATGACTCGGTATA	318				
Qy	199	GA AAA CGAGGCCCTCAGGTTCCTTTAAAAATCTCAGTCCGAGNAAGACAGAGCTGGTCCC	258				
Db	319	GAGCAGGAGCTATTTGGCTCTCTTCGGCTTGCTCAGTCTCTTAAAAACCGGCCCGGTCCA	378				
Qy	259	CCGACCCCTTTCCGCTATGTGTAGCAAGAGGATGGCCCAAACGGTGATGTCTGGTTGGGTC	318				
Db	379	CCTGAACCGTAGCGTTATGGTATTAACGNGATTGACCAACGGTGACGTTGGTTGGATT	438				
Qy	319	GAATACCTCTCTCTCAACACAACCCCTGATGTTATCTCACCCAAATCACTTTGCAATTTTC	378				
Db	439	GAGTATCTCTCTCAATGCTATCTCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	498				
Qy	379	CGAGAAAATCCTCATCATTTTCAGGGCCGTTGGGAGAACTACATTTACAGCAGTGAAGRAC	438				
Db	499	CGTCAAAACCCCTCAAAATTTTTCCGTGAGTCGGTGGAGGAGTACATGAAGGAGATTAAGGHA	558				
Qy	439	ATGTGCTATGCGGTGTTTGGAAATTCATGGCGGAGGGTTGGGGATAAGCGACAGGAATACG	498				
Db	559	GTGTCTGTA CAAGGTGTTGGAGATGGTTGCCGAAGAACTAGGGATAGACCAAGGACACT	618				
Qy	499	TTAAGCAGGTTGCTGAAGAGTGAAGAAAGTGATTCGTGCTTCAGGTTGAAACCACTACCGG	558				
Db	619	CTGAGTAAATGCTGTAGAGATGAGAAGATGACTCGTSCCTGAGACTAAACCATATTCCG	678				
Qy	559	CTTTGCCCTCAGGTGCAAGCACTGAAACCGGAATTTGGTTGGGTTTGGGAGCACACAGAC	618				
Db	679	GC---GGCGGAGGAAGAGGGCGGAAGAATGTTGAAGGTGGGGTTTGGGGAAACACACAGAC	735				
Qy	619	CCACAGATAATTCGTCTTAAAGATCTAACAGCACATCTGCTCTGCAATCTGTCTTCACA	678				
Db	736	CCACAGATAATCTCAGTGCTAAAGATCTAATAACACGGCGGGTCTTCAATCTGTGTGAAA	795				
Qy	679	GATGGCACTTTGGGTTTCAGTCCCACTGATCAGACTTCCTTTTTTCATCAATGTTGGTGAC	738				
Db	796	GATGGAAGTTGGGTGCGTGTCCCTCCTGATCACTCTTCTTCTTCTTCTTCTTCTTCTTCTT	855				
Qy	739	GCTCTACAGGTAATGATTAATGGGAGGTTTAAAAAGTGTAAAGCATAGGGTTTGGCTGAC	798				

Db	856	GCTCTTCAAGGTATGACTAAACGGGAGGTTCAGAGAGTGTAAACACACAGGGTCTTAGCCGAT	915
Qy	799	ACAACGAAGTCAAGGTTATCAATGATCTACTCTTTCGAGGACCAGCGTTCAGTGAATAATA	858
Db	916	ACAAGGAGATCGAGGATTCATGATATATTTTCGGCGGACCGCCATTTGAGCCAGAGATC	975
Qy	859	GCACCTTTACCTTCAGTGATCTTAAAGGAGAGGAGTGTTCGTTGTTCAAAAGAGTTCACATGG	918
Db	976	GCACCATTCGCCATGCTTGTCCCTGAGCAAGATGATTGGCTTTTACAAAGAATTCACCTGG	1035
Qy	919	TGTGTAATACAGAAGGCTGCGTACACTTCAGGCTAGCTGATATATAGGCTTGCCCTTTC	978
Db	1036	TCTCAATACAAATCTTCTGCTTACAAGTCTAAGCTTGGTGATTATAGACTTGGTCTCTTT	1095
Qy	979	CAGAAA 984	
Db	1096	GAGAAA 1101	
RESULT 8			
ADM94213			
ID	ADM94213	standard; cDNA; 1352 BP.	
AC	ADM94213;		
DT	17-JUN-2004	(first entry)	
DE	Soybean Dioxygenase CDNA #2.		
XX	Soybean; ss; plant; plant metabolism;		
KW	GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase;		
KW	Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase;		
KW	Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;		
KW	Ethylene response factor; Acyl-CoA thioesterase II;		
KW	ABC transporter GCN20-like; P-glycoprotein I; P-glycoprotein 3;		
KW	P-glycoprotein ATPGP; P-glycoprotein HVMDR2; ABC transporter;		
KW	PMP70 ABC transporter; MRP4 ABC transporter; transgenic.		
OS	Glycine max.		
XX	US6677502-B1.		
PD	13-JAN-2004.		
XX	12-JUL-2000; 2000US-00614912.		
XX	12-JUL-1999; 99US-0143401P.		
PR	12-JUL-1999; 99US-0143412P.		
PR	30-JUL-1999; 99US-0146650P.		
PR	15-DEC-1999; 99US-0170906P.		
PR	21-DEC-1999; 99US-0172946P.		
PR	21-DEC-1999; 99US-0172959P.		
XX	(DUPO) DU PONT DE NEMOURS & CO E I.		
PA	(PION-) PIONEER HI-BRED INT INC.		
XX	Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;		
PI	Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Caiqi PG, Fang Y;		
PI	Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;		
PI	Li CP;		
XX	WPI; 2004-088430/09.		
DR	P-PSDB; ADM94214.		
XX	New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate		
PT	synthase nucleic acid and proteins, useful for creating transgenic plants		
PT	where polypeptides are present at higher or lower levels.		
XX	Example 3; SEQ ID NO 13; 186pp; English.		
PS	The invention relates to an isolated polynucleotide comprising a		
CC	nucleotide sequence encoding a polypeptide having GTP cyclohydrolase		


```
Db 504 -----TCTCTGTTTATGCGAAAACGCTGAGAAATTTAGTGTGTTGTTGAACAGTTAC 556
Qy 421 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAATTTGATGCGGAGGGTTGGGG 480
Db 557 ATGCTCTTCTGTCAGGAAATGCGATGTGAGATCTTTGAGCTGATGCGAAGGATTAAG 616
Qy 481 ATAAGCAGAGAAATAGCTTAAGCAGGTTGCTGAGGATGAGAAAGTATTCGTGCTTC 540
Db 617 ATACACAAAAAATGTGTTAGCAAGCTTCTTATGGATAAAGAGAGTACTCTGTTTTT 676
Qy 541 AGTTGAACCACTTACCCTGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGTTGG 600
Db 677 AGGTGAATCACTACCTCTGCTTCCCTGAACTT---GTGAATGGTCAAAACATGATAGG 733
Qy 601 TTTGGGAGCACACAGACCCACAGATAATTTCTGTTTAAAGATCTAAACAGCACATCTGGC 660
Db 734 TTTGGAGAACACAGCGACCCACAAATCAITTTCTTACTTTAGGTCCAAACAATACTTCAGGC 793
Qy 661 TTGCAATCTGTCTACAGATGCGACTTGGGTTTCAGTCCACCTGATCAGACTTCTCTTT 720
Db 794 CTTCAATTTTCTTAGAGATGAAACTGGATTTTCAGTCCCACTGATCACAATCTTTTC 853
Qy 721 TTTCAATGTTGTTGAGCTCTACAGGTAATGACTTAATGGGAGGTTTAAAGTGTAAAG 780
Db 854 TTTCAATGTTGTTGAGTCTCTTCAGGTTATGACCAATGGAAGGTTTCGAAGTGTGAA 913
Qy 781 CATAGGTTTTTGGCTGACACAAACGAGTCAAGGTTATCAATGATCTACTTTTCGAGGACCA 840
Db 914 CACAGATTTTGACAAATGATTAAGTCTAGACTCAATGATTTACTTTGGAGTCCA 973
Qy 841 GGTGTTAGTGAATAATAGCACTTTTACCTTCAGTGAATTTAAAGGAGAGGAGTTTG 900
Db 974 CCAATTGAGTGAAATAATAGTACCAATTTCTTCACTATG---AAAGGAAAGAAAGCTTA 1030
Qy 901 TACAAGAGTTTCAATGGTGTGAATACAGAGGCTGCTACACTTCAGGCTAGCTGAT 960
Db 1031 TACAAGAGTTTACGTTGTTGAGTATAAAAAATTTAAACCTATGCTTCAAGATTTGGCTGAT 1090
Qy 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGT 993
Db 1091 AATAGGCTTGGACATTTTGAGAGAAATTTGTTGCT 1123

RESULT 11
AAD40262
ID AAD40262 standard; cDNA; 1403 BP.
XX AC AAD40262;
XX DT 22-OCT-2002 (first entry)
XX DE Soybean GA 2-oxidase 2 cDNA.
XX KW Gibberellin; transgenic plant; seed germination; seedling growth;
XX KW transgenic; 2-oxidase 2; enzyme; GA; soybean; gene; ss.
XX OS Glycine max.
XX FH Key Location/Qualifiers
XX FT CDS 149..1129
XX FT /*tag= a
XX FT /product= "GA 2-oxidase 2 protein"
XX PN US2002053095-A1.
XX PD 02-MAY-2002.
XX PF 10-AUG-1999; 99US-00371307.
XX PR 10-AUG-1999; 99US-00371307.
XX PA (BROW/) BROWN S M.
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XX Brown SM, Blich TD, Heck GR, Kishore GM, Logusch BW, Logusch SJ;
PI Pillier KJ, Rao S, Ream JE;
XX DR WPI: 2002-489107/52.
XX DR P-PSDB; AAE24922.
XX PT Control of gibberellin levels in plants useful to avoid unfavorable
XX PT conditions in crops to increase yields, using transgenic plants having
XX PT reduced seed germination and early seedling growth then treatment to
XX PT restore these properties.
XX PS Claim 45; Page 94-95; 155pp; English.
XX CC The invention relates to control of gibberellin (GA) levels in plants.
XX CC The method involves producing transgenic plants having a phenotype of
XX CC reduced seed germination and reduced early seedling growth, then
XX CC restoring seed germination and early seedling growth by treating plants
XX CC with an appropriate compound when conditions are favourable. The method
XX CC is useful to control seed germination and/or early seedling growth in
XX CC agricultural production so that unfavorable environmental conditions
XX CC normally reducing agronomic output can be avoided and yields increased.
XX CC Plants also demonstrate increased uniformity of germination, emergence
XX CC and seedling vigor, so increasing yields at harvest. The method is
XX CC especially useful in crop plants such as e.g. canola, soybean, cotton,
XX CC etc., and is also useful in storage and transport of seeds to reduce
XX CC premature germination which may affect agronomic or food quality of the
XX CC seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
XX SQ Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;

Query Match 42.0%; Score 418.2; DB 6; Length 1403;
Best Local Similarity 66.2%; Pred. NO. 1.7e-123;
Matches 657; Conservative 0; Mismatches 318; Indels 18; Gaps 3;

Qy 1 ATGGTTGTTCTGCTCAGCCGAGCATTTGAACCAAGTTTCTTCTGAACCATTCAGTCC 60
Db 149 ATGGTTGTTGCTGTCCAGGCCAACACAGAACAACTACTCTACATCAAGAACTACATGCCA 208
Qy 61 ACGCCCTTGTTCACGGGATTCCTGTGTGCACTTCAGCCACCCGATGCCAAGAAATCTC 120
Db 209 ACGGATTTCTCTCAACAATTTCCCGTAGTGGACCTCTCCAAACAGATGCAAGACCTTC 268
Qy 121 ATAGTGAACGCTGTGAGGACTTGGCTTCTTCAAGCTTGTGAACCATGTTTCCATG 180
Db 269 ATAGTGAAGGCTGTGAGGAAATTTGGAATTTCTCAAAAGTCATCAACCATGTTTCCCATG 328
Qy 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
Db 329 GAAACTATATCCCAATTTGGAATCTGAAGCCTTCAAGTTCTTCTATGCCACTCAATGAG 388
Qy 241 AAAGACAGAGCTGGTCCCGCCGACCCCTTTTCGCTATGTAGCAAGAGATTTGCCCAAC 300
Db 389 AAGHAAAAGTAGGCCCTCCCAACCATATGGTATGTAGCAAGAAATTTGGACACAT 448
Qy 301 GGTGATGTGGTGGTGCAGATACCTCTCTCAACACCAACCCCTGATTTATCTCACCC 360
Db 449 GGGATGTTGGTTGGTTGAGTACCTTCTCTCAACACCAATCAAGAACACAACT----- 503
Qy 361 AAATCACTTTGATTTTCCGAGAAAATCCTCATCATTTTCAGGGCGGTGGTGAGAACTAC 420
Db 504 -----TCTCTGTTTATGGCAAAAACGCTGAGAAATTTAGGTGTTTGTGAACAGTTAC 556
Qy 421 ATTACAGCAGTGAAGAACATGCTGCTATGCGGTGTTGGAATTTGATGCGGAGGGTTGGGG 480
Db 557 ATGCTCTTCTGAGGAAATTTGAGATTTCTTGAAGTATTTAGCTGATGCGAAGATTAAG 616
Qy 481 ATAAGCAGAGAAATACCTTAAGCAGGTTGCTGAGGATGAGAAAGTATTCGTGCTTC 540
Db 617 ATACACAAAAAATGTGTTTAGCAAGCTTCTTATGGATAAAGAGAGTACTCTGTTTTT 676
Qy 541 AGTTGAACCACTTACCCTGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGTTGG 600
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Db 677 AGGTGAATCACTACCTGCTGCCCTGAACCTT---GTGAATGGTCAAAACATGATAGGG 733
QY 601 TTTGGGGAGCACACAGACCCACAGATAAATTTCTGTCTTAAGATCTTAACAGCACATCTGGC 660
Db 734 TTTGGAGAACACAGGACCCACAAATCAATTTCTACTTAGTTCACACATATCTCAGGC 793
QY 661 TTGCAAAATCTGTCTCAGAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTT 720
Db 794 CTTCAGATTTTCTTAGAGATGAAACTGGATTTCACTCCCACTGATCACAATCTTTC 853
QY 721 TTCAATCAATTTGGTACGCTCTACAGTAATCACTAATGGGAGGTTTAAAGTGTAAAG 780
Db 854 TTCAATAATTTGGTGATTTCTTTCAGGTTATGCAATGGAAGGTTTCAAGTGTGAA 913
QY 781 CATAGGTTTTGGCTGACACCAACCAAGTCAAGGTTTCAATGATCTACTTTGGAGGACCA 840
Db 914 CACAGAGTTTGGCAAAATGGAATTAAGTCTAGACTCTCAATGATTTACTTTGGAGTCCA 973
QY 841 GCCTTGAAGTGAATAATAGCACCTTTTACCTTTCAGTGTATGTTAAAGGAGGAGTGTG 900
Db 974 CCATTGAGTGAGAAATAGTACCATTTATCTTCACTTATG---AAAGGAAAGAAAGCTTA 1030
QY 901 TACAAGAGTTTCACTGCTGTGAATACAGAAGCTGCTGATCACTTCAAGGCTAGCTGAT 960
Db 1031 TACAAGAGTTTACGTTGGTTCGAGTATATAAAATTTAACTTATGCTTCAAGATTGGCTGAT 1090
QY 961 AATAGGCTTGCCCTTTCCAGAAATCTGCTGCT 993
Db 1091 AATAGGCTTGACATTTTGAGAGAAATTTGTTGCT 1123

RESULT 12
ID AAZ55917 standard; DNA; 1008 BP.
XX AAZ55917;
XX 10-APR-2000 (first entry)
XX Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox3 DNA.
XX Gibberellin 2-oxidase; AtGA2ox3; 2-beta-hydroxylation; inactivation;
KW growth inhibition; ds.
XX Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 1..1008
FT /tag= a
FT /product= "Gibberellin 2-oxidase AtGA2ox3"
XX WO966029-A2.
XX 23-DEC-1999.
XX 11-JUN-1999; 99WO-GB001857.
XX 12-JUN-1998; 98GB-00012821.
XX 15-JUL-1998; 98GB-00015404.
XX (UYBR-) UNIV BRISTOL.
XX Thomas SG, Hedden P, Phillips AL;
XX WPI; 2000-097742/08.
DR P-PSDB; AAY58600.
XX New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
PT to produce transgenic plants with improved or altered growth
PT characteristics.
XX Example 3; Fig 9; 42pp; English.
PS
XX

CC This sequence represents cDNA encoding an Arabidopsis thaliana
CC gibberellin (GA) 2-oxidase, PCGA2ox3. This enzyme is a GA 2-beta-
CC hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is
CC its only activity. Hydroxylation at the 2-beta position of a GA results
CC in a biologically inactive product, and is the most important route for
CC GA metabolism in plants, ensuring that the active hormones do not
CC accumulate in plant tissues. The nucleic acids can be used to transform
CC plants so that gibberellin 2-oxidase can be constitutively over-expressed
CC or otherwise enhanced to reduce the concentration of bioactive GA in the
CC plants and therefore to inhibit plant growth. Growth inhibition is useful
CC in many agricultural and horticultural applications such as enhancing
CC lodging-resistance and grain yield in cereals, improving seedling
CC quality, reducing the growth of amenity grasses, reducing shoot growth in
CC orchard and ornamental trees, improving tolerance to cold, drought and
CC infection, and increasing yields (by the diversion of assimilates from
CC vegetative to reproductive organs). The nucleic acids may also be used to
CC induce male and/or female sterility (by expression in floral organs),
CC prevent pre-harvest sprouting, reduce shoot growth in hedging plants,
CC inhibit reversibility in the development or germination of seeds and
CC reduce shoot growth in commercial wood species. Antisense constructs of
CC the nucleic acids can also be used to transform plants to reduce the
CC expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
CC improve fruit set and growth in seedless grapes, citrus fruits and
CC pears), improve skin texture and fruit shape in apples, increase stem
CC length and therefore yield in sugar cane, increase yield and earliness in
CC celery and rhubarb, improve malting yields and quality in cereals
CC (particularly barley), and increase growth in woody species
XX
XX Sequence 1008 BP; 296 A; 212 C; 232 G; 268 T; 0 U; 0 Other;
SQ
Query Match 38.3%; Score 381.6; DB 3; Length 1008;
Best Local Similarity 64.7%; Pred. No. 9.2e-112;
Matches 586; Conservative 0; Mismatches 314; Indels 6; Gaps 1;
QY 79 ATTCTGTGGTGCAGCTCAAGCACCAGGATCCAGAGAAATCTCATAGTGAACGCTGTAGG 138
Db 79 ATCCCTGTTATAGACTTAACCGACTCAGATGCCAAACCCAAATCGTCAAGGCATGTGAA 138
QY 139 GACTTGGGCTCTTCAAGCTTGTGAACCATGTTTCCATTGGAGTTAATGGCAATTTA 198
Db 139 GAGTTTGGGTTCTTCAAGTCAATCAACCATGGGTCGACCCGATCTTTGACTCAGTTG 198
QY 199 GAAACGAGGCGCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC 258
Db 199 GAGCAAGAGCCATCAACTTCTTTGCTTTCATCACTCTCTCAAGACAAAGCGGTCCA 258
QY 259 CCGACCCCTTCGGCTATGTTAGCAAGAGGATGGCCAAACGGTGATCTCGTTGGGTC 318
Db 259 CCGACCCCTTCGGTTACGTTACTAAAGGATTTGGACCCCAATGGTGACCTTGGCTGGCTT 318
QY 319 GAATACCTCTCTCAACACCAACCTGATGTTTATCTCAACCCCAATCACTTTTGCAATTTTC 378
Db 319 GAGTACATTTCTTAAATGCTAATCTTTGCTTGAGTCTCACAAAACCCACCGCATTTTC 378
QY 379 CGAGAAAATCCTCATCATTTTCAGGGCGGTGGTGGAGAACTACATTCACAGCTGGAAGAAC 438
Db 379 CGGCACACCCCTGCAATTTTCAGAGAGGCGAGTGAAGAGTACATTTAAAGAGATGAAGAGA 438
QY 439 ATGTGCTATGCGGTGTGGAAATTTGATGGCGAGGGGTTGGGGATTAAGGCAGAGGAATACG 498
Db 439 ATGTGAGCAAAATTTCTGGAATTTGTAGAGGAAGAGCTAAAGATAGAGCCAAAGGAGAAAG 498
QY 499 TTAAGCAGGTTCTGAAGGATGAGAAAAGTGAATTCGTGCTTCAGGTTGAACCACTACCCG 558
Db 499 CTGAGCCGTTTGGTGAAGTGAAGAAAGTGAATTCGTGCTTGAGAAATGAACCAATTTACCCG 558
QY 559 CCTTGGCCCTGAGGTGCAAGCACTGAACCCGGAATTTTGGTTGGGTTTGGGGAGCACACAGAC 618
Db 559 -----GAGAAGGAGAGACTCCGGTCAAGGAAGAGATTGGGTTGCTGAGCACACTGAT 612
QY 619 CCACAGATAAATTTCTGTCTTTAAGATCTAAACAGACATCTGGCTTGCAAAATCTGTCTCACA 678
Db 613 CCACAGTTGATATCACTGCTCAGATCAACACGACACAGAGGGTTTGCATAATCTGTGTCAAA 672

Db	488	CTGCGCCGCTCCGTCCTCGC-----CGCTCTCCGGGCGGCGCTGAACGATACA	538	PR	08-APR-1999;	99US-0128714P.
QY	422	TTACACAGTGAAGAACATGTGCTATGCGTGTTCGAAATTGATGGCGGAGGGTTGGGGA	481	PR	16-APR-1999;	99US-0129845P.
Db	539	TCGCGCGGTGCGAAGGTGGCGGTGCGGTGATGAGGGGATGGCGGAGGGCTGGGCA	598	PR	19-APR-1999;	99US-0130077P.
QY	482	TAAGGCAGAGGAATACGTTAAGCAGGTTCGTGAAGGATGAGAAAAGTGATTGCTGCTTCA	541	PR	21-APR-1999;	99US-0130449P.
Db	599	TTGCGGCCGTGGACGCGCTGAGCGGATGCTGACGCGGAGGGGACCGCAGGTGTTCC	658	PR	23-APR-1999;	99US-0130510P.
QY	542	GGTTGAACACATACCCGCTTCGCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGT	601	PR	23-APR-1999;	99US-0130891P.
Db	659	GGGTGAACCACTACCCGCGCTGCCACGCGTGCAGGGGCTGGGCTGCAGCGCCACCGGCT	718	PR	28-APR-1999;	99US-0131449P.
QY	602	TTGGGGAGCACACAGACCCACAGATAATTTCTGCTTTAAGATCTAACACGACATCTGGCT	661	PR	28-APR-1999;	99US-0132048P.
Db	719	TCGGCGAGCACACGGACCGCGACGCTCATCTCGTGTGCGCTCCAAACGGCAGCGTCGCGGC	778	PR	28-APR-1999;	99US-0132407P.
QY	662	TGCAAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCCACCTGATCAGACTTCCCTTT	721	PR	30-APR-1999;	99US-0132484P.
Db	779	TGCAGATCGGCTCCAGAACGGCAGTGGGTGTCGCTGCCCTCGGACCGGACGCTTCT	838	PR	05-MAY-1999;	99US-0132485P.
QY	722	TCATCAATGTTGTGACGCTCTACAGGTAAATGACTAATGGAGGTTTAAAGTGTAAGC	781	PR	06-MAY-1999;	99US-0132486P.
Db	839	TCGTCAACGTCGGCGACTCGTTGCAGGTGCTGACCAACGGGAGGTTCAAGAGCGTGAAGC	898	PR	07-MAY-1999;	99US-0132487P.
QY	782	ATAGGGTTTTGGCTGACACACGAACTCAAGTTATCAATGATCTACTTTGGAGGACCAAG	841	PR	11-MAY-1999;	99US-0132563P.
Db	899	ACAGGGTGGTGGCCACAGCCTTAAGTCTAGGGTTTCCATGATCTACTTTGGAGGCGCAG	958	PR	11-MAY-1999;	99US-0132863P.
QY	842	CGTTGAGTGAAATATAGCACCTTTTACCTTTCAGTGTATGTTTAAAGGAGAGGAGTGTTCGT	901	PR	14-MAY-1999;	99US-0134218P.
Db	959	CGATGACACAGAGGATTCACCATTCGCCAGCTGCTGGCGCGGAGAGCAGAGCTGT	1018	PR	14-MAY-1999;	99US-0134219P.
QY	902	ACAAAGATTTCATGGTGTGAATAACAAGAGCTGCGTACACTTCAAGGCTAGCTGATA	961	PR	14-MAY-1999;	99US-0134221P.
Db	1019	ACAAGGACTTCATATGGGCGAGTACAAGAAGGCTGCTACAACTCCAGGCTCGGGGACA	1078	PR	14-MAY-1999;	99US-0134370P.
QY	962	ATAGGCTTGCCCTTTCCAGA	982	PR	14-MAY-1999;	99US-0134370P.
Db	1079	ACAGGCTGGCTAGTTCACCA	1099	PR	18-MAY-1999;	99US-0134941P.
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XX	AAC39277;					99US-0136021P.
AC	XX					99US-0136392P.
DT	17-OCT-2000 (first entry)					99US-0136782P.
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 24035.					99US-0137222P.
DE	XX					99US-0137528P.
XX	Hybridisation assay; genetic mapping; gene expression control;					99US-0138047P.
KW	protein identification; signal transduction pathway; metabolic pathway;					99US-0138454P.
KW	promoter; termination sequence; ss.					99US-0138455P.
XX	OS					99US-0138456P.
OS	Arabidopsis thaliana.					99US-0138457P.
XX	EP1033405-A2.					99US-0138461P.
PN	XX					99US-0138462P.
PD	06-SEP-2000.					99US-0138463P.
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PR	25-OCT-1999;	99US-0161406P.
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Query Match 35.8%; Score 356.6; DB 3; Length 1224;		
Best Local Similarity 63.2%; Pred No. 1.2e-103;		
Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;		
QY	65	CCTTGTTCACGGGGATTCCTGTGGTGCACCTTCACGACCCCGATGCCAAGAATCTCATAG 124
DB	99	CGGGTTCTCTCTAATCCGGTTATAGATATGTCTGACCCAGAAATCCAAACATGCCCTCG 158
QY	125	TGAACGCCGTGAGGACTTCGGCTTCTTCAAGCTTGTGACCATGCTGTTCATTTGGAGT 184
DB	159	TGAAGACATGCGAAGACTTCGGCTTCTTCAAGGTGATCAACCATGCGTTTCGGCAGAGC 218
QY	185	TAATGGCCAATTTAGAAACGAGGCCCTCAGGCTCTTTTAAAAAATCTCAGTCCGAGAAAG 244
DB	219	TAGTCTCTGTTTTAGAACACGAGACGTCGATTTCTTCTCGTTGCCAAGTCAGAGAAA 278
QY	245	ACAGAGCTGTGTCCTCCCGACCCCTTTCCGCTATGGTAGCAAGAGATTGCCCAACCGTG 304
DB	279	CCCAAGTCG---CAGGTTATCCCTTAGGATACGGGAACAGTAAGATTGGTCGGAATGGTG 335
QY	305	ATGTCGGTTGGTGCAGATACCTCTCTCAACACCAACCCCTGATGTTATCTACCCAAAT 364
DB	336	ACGTGGGTTGGGTTGAGTACTTTGTTGATGAACGCTAATCTTGATTCGGGTCGGTCCAC 395
QY	365	CACTTTGCATTTTCCGAGAAAATCCTCATCATTTTCAGGCGGTGGTGAGAACTACATTA 424
DB	396	TATTTCCAAGTCTTCTCAAAAGCCGGGAACCTTCAGAAACGATTTGGAGAGTACACAA 455
QY	425	CAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATTTGATGGCGGAGGGTTGGGGATAA 484
DB	456	CATCAGTGAGAAAATGACATCGATGTTTTCGAGAGAATCACAGATGGCTAGGGATCA 515
QY	485	GGCAGAGGAATACGTTTAAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTCAGGT 544
DB	516	AACCGAGGAACACACTTAGCAAGCTTGTGTCTGACCCAAACACGGACTCGATATTGAGAC 575
QY	545	TGAACCACTACCGCTTGCCTGAGGTGCAAGCACTGAAC-----CGGAATTTGG 595
DB	576	TTAATCATTATCCACATGCTCTTTAGCAATAAGAAAACCAATGGTGGTAGAATGTGA 635
QY	596	TTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGACAT 655
DB	636	TTGGTTTGGTGAACACACAGATCTTCAAAATCATCTCTGTCTTAAGATCTTAACACACTT 695
QY	656	CTGGCTTGCAAAATCTGTCTCAAGATGGCACTTGGGTTTCAGTCCCACTGATCACACTT 715

Db	696	CTGGCTCCAAATTAACTTAAATGATGGCTCATGGATCTCTGTCCCTCCCGATCACACTT	755
Qy	716	CTTTTTTCATCAATGTGGTGCCTCTACAGGTAATGACTAAATGGGAGGTTTTAAAAGTG	775
Db	756	CTCTCTCTTCCAAAGCTGGTGACTCTCTCCAGGTGATGACAAATGGGAGGTTCAAGAGCG	815
Qy	776	TAAAGCATAGGTTTTGGCTGCACACAACGAAGTCAAGGTTATCAATCATCTACTTTGGAG	835
Db	816	TGAGGCATAGGTTTTAGGCTAACTGTAAAGAAATCTAGGGTTTCTATGATTTACTTTCGCTG	875
Qy	836	GACCAGCGTTGAGTGAATAATAGACACCTTTTACCTTCAGTGAATGTTAAAAAGGAGAGAGT	895
Db	876	GACCTTCATTGACTCAGAGAATCGCTCCGTTGACATGTTTGATAGACAATGAGCAGAGA	935
Qy	896	GTTTGTACAAAGAGTTTCACATGGCTGTAATACAGAGGCGCTGTACACTTCAAGGCTAG	955
Db	936	GGTTGTACAGAGAGTTTACTTGGTCTGAATACAAAATCTTACCTCAACTCTAGATTGT	995
Qy	956	CTGATAATAGGCTTGCCCTTTTCCTCCAGA	982
Db	996	CTGATAATAGGCTTCAACAATTCGAAA	1022

RESULT 15
AAZ55915
ID AAZ55915 standard; cDNA; 1316 BP.
XX
XX
AC AAZ55915;
XX
XX
DT 10-APR-2000 (first entry)
XX
DE Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox1 cDNA.
XX
XX
KW Gibberellin 2-oxidase; AtGA2ox1; 2-beta-hydroxylation; inactivation;
KW growth inhibition; ss.

	Key	Location/Qualifiers
FT		41..1030
PT		/tag= a
PT		/product= "gibberellin 2-oxidase AtGA2ox1"
FT		

PN WO9966029-A2.

PD 23-DEC-1999.

11-JUN-1999; 99WO-GB001857.

PR 12-JUN-1998: 98GB-00012821-XX

PR 15-JUL-1998; 98GB-00015404.

PA (UYBR-) UNIV BRISTOL.

PI Thomas SG, Hedden P, Phillips AL;

WPI; 2000-097742/08.

DR P-PSDB; AAY58598.

PT New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.

PS Example 3: Fig 5: 42pp: English.

CC This sequence represents cDNA encoding an Arabidopsis thaliana
CC gibberellin (GA) 2-oxidase, PGCA2ox1. This enzyme is a GA 2-beta-
CC hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is
CC its only activity. Hydroxylation at the 2-beta position of a GA results
CC in a biologically inactive product, and is the most important route for
CC GA metabolism in plants, ensuring that the active hormones do not
CC accumulate in plant tissues. The nucleic acids can be used to transform
CC plants so that gibberellin 2-oxidase can be constitutively over-expressed

or otherwise enhanced to reduce the concentration of bioactive GAS in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), prevent pre-harvest sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species (e.g., poplar).

Sequence 1316 BP: 440 A; 249 C; 252 G; 375 T; 0 U; 0 Other; XX

Query Match	35.8%	Score	356.6;	DB 3;	Length	1316;			
Best Local Similarity	63.2%	Pred. No.	1.2e-103;						
Matches	586;	Conservative	0;	Mismatches	329;	Indels	12;	Gaps	2;

Qy	65	CTTTGTTTCA CGGGGATTCCTGTGTTGACCTCA CGCACCCCGATGCCAAGAATCTCATAG	124
Db	78	CCGGTTTCTCTCTAATCCGGTTTATAGATATGTCTGACCCAGAATCCAACATGCCCTCG	137
Qy	125	TGAACGCTGTGAGGACTTCGGCTTCTTCAAGCTTTGTCAACCATGGTGTTCATTTGGAGT	184
Db	138	TGAAGAATGCGAAGACTTCGGCTTCTTCAAGGTGATCAACCATGGCGTTTCCGAGAGC	197
Qy	185	TAATGGCCAAATTTAGAAAAAGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAG	244
Db	198	TAGTCTCTGTTTATAGAACACAGAGACCGTCCGATTTCTTCTCGTTGCCAAGTCAGAGAAAA	257
Qy	245	ACAGAGCTGGTCCCCCGACCCCTTTCGGCTATGTAGCAAGAGGATTCGCCCAACGGTG	304
Db	258	CCCAAGTCG---CAGGTATCCCTTCGGATACGGAA CAGTAAGATTTGGTCCGAATGGTG	314
Qy	305	ATGTGCGTGTGGGTCCGAATACCTCCTCTCAACACCAACCCCTGATGTTATCTCACCCAAT	364
Db	315	ACGTGGGTGGGTGAGTACTTTGTTGATGAACGCTTAATCATGATTCCTCGGTTCCGGTCCAC	374
Qy	365	CACTTTCGATTTTCCGAGAAAATCCTCATATTTTCAGGCGGTGGTGAGAACTACATTTA	424
Db	375	TATTTCCAAGTCTTCTCAAAAGCCCGGAACTTTTCAGAAAACGATTTGAAGAGTACACAA	434
Qy	425	CAGCAGTGAAGAAACATGTGCTATGCGGTGTGGAATTCATGGCGGAGGGTTGGGGATAA	484
Db	435	CATCAGTGAAGAAAATGACATTCGATGTTTGGAGAAATCACAGATGGGCTAGGATCA	494
Qy	485	GGCAGAGGAATACTTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGT	544
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Qy	545	TGAACCACTACCGCCCTTGCCCTCAGGTTGCAAGCACTGAAC-----CGCAATTTGG	595
Db	555	TTAATCACTATCCACCATGTCTCTTAGCAATAAGAAAACCAATGGTGGTAGAATGTGA	614
Qy	596	TTGGTTTGGGAGCACACAGACCCACAGATAAATTTCTGTCTTAAGATCTAA CAGACAT	655
Db	615	TTGGTTTGGTGAACACACAGATCCTCAAAATCATCTCTGTCTTAAAGATCTTAACAACATT	674
Qy	656	CTGGCTTCGAAATCTGTCTCACAGATCGCACTTGGGTTTTCAGTCCCACTGATCAGACTT	715
Db	675	CTGGTCTCCAAATTAATCTAANTGATGCTCATGGATCTCTGTCTCCTCCGATCACACTT	734
Qy	716	CTTTTTTCACTAATGTTGGTGACGCTCTACAGGTAAATGACTAAATGGGAGGTTTAAAAGTG	775
Db	735	CTTCTTTCTTCAACGGTTGGTACTCTCTCCAGGTGATGACAAATGGGAGGTTCAAGAGCG	794

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 17:35:38 ; Search time 4543.12 Seconds
(without alignments)
10257.253 Million cell updates/sec

Title: US-10-670-454-1_COPY_68_1063

Perfect score: 996
Sequence: 1 atggtgtctgtctcagcc.....tcagaaatctgctgtgat 996

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_est4:*
- 5: gb_est5:*
- 6: gb_est6:*
- 7: gb_est7:*
- 8: gb_est8:*
- 9: gb_est9:*
- 10: gb_est10:*
- 11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	45.6	653	AW184969	se84f09.y
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4	424.4	42.6	1362	CNS0ABST	EX816963 Arabidops
5	421.2	42.3	1141	CNS09YVQ	EX841768 Arabidops
6	420.4	42.2	622	BU549366	BU549366 GM880016A
7	416.4	41.8	1363	CNS0ABKL	EX815974 Arabidops
8	386.4	38.8	1339	CNS0AC3R	EX814383 Arabidops
9	375.6	37.7	612	BE802903	BE802903 sr46c09.y
10	355.8	35.7	785	AJ803092	AJ803092 AJ803092
11	348.6	35.0	1128	CNS0ADWT	EX814091 Arabidops
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13	334.8	33.6	567	BM893076	BM893076 sam51f05.
14	332.8	33.4	478	AL382874	AL382874 MCB10E02
15	329.2	33.1	893	DN589159	DN589159 50141.1 L
16	323.4	32.5	792	BI935635	BI935635 EST555524
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18	307.2	30.8	625	CV292693	CV292693 EST81070
19	307.2	30.8	642	CV292668	CV292668 EST81045
20	305.6	30.7	438	BP940509	BP940509 BP940509
21	305.6	30.7	755	BM690134	BM690134 BM690134
22	305.6	30.7	776	BM692820	BM692820 BM692820

C 23	305.6	30.7	779	3	BJ571134	BJ571134
C 24	303.6	30.7	808	3	BJ575888	BJ575888
C 25	303.6	30.5	529	2	BG881784	BG881784
C 26	303.6	30.5	663	7	CV292717	CV292717
C 27	300.6	30.2	753	3	BI968577	BI968577
C 28	300.6	30.1	743	2	BG646259	BG646259
C 29	298.2	29.9	789	5	BM685035	BM685035
C 30	293.8	29.5	517	3	BP074757	BP074757
C 31	293.8	29.5	520	3	BP074168	BP074168
C 32	292.6	29.4	579	6	CA844444	CA844444
C 33	292.6	29.4	724	6	CA844443	CA844443
C 34	288.6	29.0	847	8	DN982067	DN982067
C 35	287	28.8	619	1	AW584268	AW584268
C 36	286.6	28.8	789	7	CV470333	CV470333
C 37	279.8	28.1	611	1	AW309039	AW309039
C 38	279.4	28.1	501	3	BP060951	BP060951
C 39	278.4	28.0	604	7	CV630114	CV630114
C 40	277.6	27.9	853	7	CV469374	CV469374
C 41	273.6	27.5	800	3	BI970132	BI970132
C 42	273	27.4	685	2	BG523146	BG523146
C 43	273	27.4	698	8	DR399076	DR399076
C 44	272.2	27.3	711	1	AW222239	AW222239
C 45	270.6	27.2	655	5	BQ404995	BQ404995

ALIGNMENTS

RESULT 1
AW184969
LOCUS
DEFINITION
se84f09.y1 Gm-cl023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl023-1410 5' similar to TR:O04162 O04162 DIOXYGENASE. i, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AW184969
AW184969.1 GI:6454286
EST.
Glycine max (soybean)
Glycine max

REFERENCE
AUTHORS
1 (bases 1 to 653)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Other ESTs: BU544870 corresponding to Gm-cl088-979 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: es@wustl.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert length: 1472 Std Error: 0.00
High quality sequence stop: 436.

FEATURES
source
1..653
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="T157"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl023-1410"

/tissue_type="seed coats of greenhouse grown plants"
/lab_host="DH10B"
/clone_lib="Gm-cl023"
/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
cDNA library was constructed from mRNA isolated from seed
coats (100-200mgs) of greenhouse grown plants. The
library was prepared using the Life Technologies
pSuperScript cDNA library construction kit. Complementary
DNA was synthesized from mRNA using a poly (dT) sequence
with a Not I restriction site. Sal I linkers adapters
were ligated to the blunt-ended cDNA fragments followed by
Not I digestion. The cDNA fragments were directionally
cloned into the Not I-Sal I restriction site of the
pSPORT1 vector. The ligated cDNA fragments were
transformed into E.coli Electromax DH10B host cells. This
library was constructed by Dr. Lila Vodkin and Dr. Anu
Khanna."

ORIGIN

Query Match 45.6%; Score 454; DB 1; Length 653;
Best Local Similarity 87.2%; Pred. No. 1.8e-127;
Matches 496; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 1 ATGGTTGTTCTGTCTCAGCCAGCATTTGAACAGTCTTTCTCTGAAACCATTCCTCAAGTCC 60
DB 84 ATGGTTGTTCTGTCTCAGCCAGCATTTGAACAGTCTTTCTCTGAAACCATTCCTCAAGTCC 143
QY 61 AGCCCTCTGTCTCAGCGGGATTCCTGTGTCGACCTCAGCCACCCCGATGCCAGATCTC 120
DB 144 AGCCCTCTGTCTCAGCGGGATTCCTGTGTCGACCTCAGCCACCCCGATGCCAGATCTC 203
QY 121 ATAGTGAAGCCCTGTAGGAGCTTCGGCTCTCTCAAGCTGTGAACCATGGTGTCTCCATTG 180
DB 204 ATAGTCAATGCCCTGAGGAGCTTCGGCTCTCTCAAGCTGTGAACCATGGTGTCTCCATTG 263
QY 181 GAGTTAATGGCCAAATTAGAAAACGAGGCGCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
DB 264 CAGTTTCATGGCCAAATTGGAAAACGAAACCCCTCGGTTCTTCAAAAAACCTCAATCCGAG 323
QY 241 AAAGACAGAGCTGGTCCCCCGACCTTCGGCTATGTTAGCAGAGGATTTGGCCCAAC 300
DB 324 AAAGACAGGCTGGTCCCCCGACCTTCGGCTATGTTAGCAGAGGATTTGGCCCAAC 383
QY 301 GGTGATGTCGGTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTATCTCAACC 360
DB 384 GGGATGTCGGTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTATCTCAACC 443
QY 361 AATCATCTTTGCAATTTCCGAGAAAATCTCTATCATTTTCAGGCGGTGGTGGAGAACTAC 420
DB 444 AAGTCACAGTTTCATTTTCAGAGAAGGTCCTCAGAAATTCANGGCGGTGGTGGAGGAATAC 503
QY 421 ATTACACAGTGAAGACATGTCTATGCGGTGTTGGAATTCATGCGGAGGGTGGG 480
DB 504 ATTAGAGCGGTGAAGAACATGTCTATGAGGTGTTGGAATTCATGCGTGAAGGATTTGG 563
QY 481 ATAAGCAGAGGAATACGTTTAAGCAGGTGTCTGAAGGATGAGAAAAGTATTCGTCTTC 540
DB 564 ATAAACCATAGGATGTTGTAGTATGTTGCTGAACGATGAGAGAGTATCTTCTGCTTC 623
QY 541 AGGTTGAACATACCCCGCTTGCCTGA 569
DB 624 AGACNTTACCACTACCCCGCATTCGCGGA 652

RESULT 2

BM085298 566 bp mRNA linear EST 23-JUL-2004
LOCUS saj34h07.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ; mRNA
sequence.
ACCESSION BM085298
VERSION BM085298.1 GI:16995926
KEYWORDS EST.

SOURCE
ORGANISM

Glycine max (soybean)
Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 566)

Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Corvett,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.

TITLE
JOURNAL

Public Soybean EST Project

COMMENT

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 426.

FEATURES

source

1..566
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl066-4957"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week
old seedling"
/lab_host="DH10B"
/clone_lib="Gm-cl066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedling from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

ORIGIN

Query Match 44.5%; Score 443.4; DB 3; Length 566;
Best Local Similarity 88.0%; Pred. No. 3.1e-124;
Matches 493; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 1 ATGGTTGTTCTGTCTCAGCCAGCATTTGAACAGTCTTTCTCTGAAACCATTCCTCAAGTCC 60
DB 18 ATGGTTGTTCTGTCTCAGCCAGCATTTGAACAGTCTTTCTCTGAAACCATTCCTCAAGTCC 77
QY 61 AGCCCTCTGTCTCAGCGGGATTCCTGTGTCGACCTCAGCCACCCCGATGCCAGATCTC 120
DB 78 AGCCCTCTGTCTCAGCGGGATTCCTGTGTCGACCTCAGCCACCCCGATGCCAGATCTC 137
QY 121 ATAGTGAAGCCCTGTAGGAGCTTCGGCTCTCTCAAGCTGTGAACCATGGTGTCTCCATTG 180
DB 138 ATAGTGAAGCCCTGTAGGAGCTTCGGCTCTCTCAAGCTGTGAACCATGGTGTCTCCATTG 197
QY 181 GAGTTAATGGCCAAATTAGAAAACGAGGCGCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240

Db 198 GAGTTTCATGGCCAAATTTGGAAACGAAACCCCTCAGGTTCTTCAAAAAACCTCAGTCCGAC 257
Qy 241 AAAGCAGAGCTGGTCCCGCCGACCTCTTCGGCTATGGTAGCAGAGGATTCGCCCAAC 300
Db 258 AAAGCAGAGGCTGGTCCCGCCGATCTTTGGCTACGGCAGGAGGATTCGCCCTAAC 317
Qy 301 GGTGATGTCGGTGGGTGGAATACCTCTCCCTCAACACCAACCCCTGATTTATCTCACCC 360
Db 318 GCGGATGTCGGTGGGTGGAATACCTCTCTCAACACCAACCCCTGATCTATCTCCGCC 377
Qy 361 AAATCACCTTTCATTTCCGAGAAATCCTCATCTTTTCAGGCGGTGGTGAGACTAC 420
Db 378 AAGTCACAGTTCATTTTCGAGAAAGTCTCAGAATTTTCAGGGTGGTGGTGGAGATAC 437
Qy 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGGTGGAAATTCATGCGGAGGGGTGGGG 480
Db 438 ATTAGGCGCTGAGNACATGTGCTATGAGGTGGTGGAAATTAATGGCGAGGGCTTGGGA 497
Qy 481 ATAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTATTCGTGCTTC 540
Db 498 ATAATCAGAGGAATGCGTTGAGTAGTGGTTCGTAAGGATGAGAAGTATTCCTGCTTC 557
Qy 541 AGGTTGAAC 549
Db 558 AGACTTAAC 566

RESULT 3
CNSOAC6N 1365 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLTFB7ZE01 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).
ACCESSION BX814544
VERSION BX814544.1 GI:42472102
SOURCE HTC; GSLT cDNA.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1365)
Castelli, V., Aury, J.M., Jallou, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Queller, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1365)
Genoscope.
JOURNAL Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallou O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.

FEATURES
source Location/Qualifiers
1..1365
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
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gene
ORIGIN
Query Match 42.7%; Score 424.8; DB 4; Length 1365;
Best Local Similarity 67.2%; Pred. No. 2.1e-118;
Matches 516; Conservative 0; Mismatches 297; Indels 3; Gaps 1;
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/tissue_type="Flowers and buds"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
1..1365
/gene="Atlg30040"

Qy 79 ATTCTGTGTGCGACTCAGCACCCCGATCGCAAGAAATCTCATAGTGAACCCCTGTAGG 138
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Qy 139 GACTTCGGCTTCTTCAAGCTTGTGAACCATGCTGTTCCATTGGAGTTAATGSCCAATTTA 198
Db 255 GAGTTTCGGGTCTTCAAGGTGCTAAACCAACGAGGTCCGACCCGAACTCATGACTCGTTA 314
Qy 199 GAAAAAGAGGCGCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGCTCC 258
Db 315 GAGCAGGAGGCTATTTGGCTTCTTCGGCTTGCCTCAGTCTCTTAAAAACCGGCCGTTCA 374
Qy 259 CCCGACCTTTTCGGCTATGTAGCAAGAGGATTTGCCCAAAACGGTGTATGTCGGTTGGGTC 318
Db 375 CCGAACCGTACGGTTATGGTAAATAACGGATTGGACCAACCGTGACGCTTGGTTGGATT 434
Qy 319 GAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCACCAATCATTTGCAATTTTC 378
Db 435 GAGTATCTCTCTCAATGCTAAATCCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494
Qy 379 CGAGAAAAATCTCATCATTTTCAGGCGGTGGTGAGAACTACATTACAGCAGTGAAGAAC 438
Db 495 CGTCAACCCCTCAAAATTTTCGGTGAAGTGGTGGAGGATACATGAAGAGATTAAAGAA 554
Qy 439 ATGTGCTATGCGGTTCGAAATTTGATGGCGAGGGTTGGGATAGGAGGAGGAAATAGC 498
Db 555 GTGTGCTACAAAGTGTTCGAGATGTTCCGGAAGAACTAGGGATAGAGCAAGGACACT 614
Qy 499 TTAAGCAGGTTGCTGAAGGATGAGAAAGTATTCGTGCTTCAGGTTGACCACTACCCG 558
Db 615 CTGAGTAAATGCTGAGAGATGAGAAAGTGAAGTCTGCTGCTGAGACTAAACCATTTATCCG 674
Qy 559 CTTGCCCTGAGGTCCAAAGCACTGAACCGGAATTTGGTGGGTGGGAGGAGCAGACAGAC 618
Db 675 GC---GGCGGAGGAGAGCGCGGAGAGATGGTGAAGTGGGGTTTGGGGAACACAGAC 731
Qy 619 CCACAGATAATTTCTGCTTAAGATCTAACAGCAATCTGGCTTGCAAAATCTGTCTCACA 678
Db 732 CCACAGATAATCTCAGTGTCTAAGATCTAATAACAGCGGGGTCTTCAAAATCTGTGTGAAA 791
Qy 679 GATGCACCTTGGGTTTCAGTCCCACTGATCAGACTTCTTTTTCATCAATCTTGGTGAC 738
Db 792 GATGGAAGTTGGGTTCGCTGCTCCCTCTGATCACTCTTCTTCTTCAATTAATGTGGAGAT 851
Qy 739 GCTCTACAGGTAATCACTAAATGGGAGGTTTAAAGGTAAAGCATAGGGTTTGGCTGAC 798
Db 852 GCTCTTACAGTTATGACTAAACCGGAGGTTCAAGAGTGTAAACACAGGGCTTAGCCGAT 911
Qy 799 ACAACGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAACCGGTTGAGTGAAATATA 858
Db 912 ACAAGGAGATCGAGGATTTCAATGATATATTTTCGGCGGACCCCATTTGAGCCAGAGATC 971
Qy 859 GCACCTTTACCTTACGATGTTAAAGAGGAGGAGTGTGTTGTACAAAGATTCACATGG 918
Db 972 GCACCATTTGCCATGCTTGTCTCCCTGAGCAAGATGATGGCTTTTACAAAGAAATTCATTG 1031
Qy 919 TGTGTAATCAAGAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCTCTTC 978
Db 1032 TCTCAATCAAAATCTTCTGCTTACAAAGTCTAAGCTTGTGATATAGACTTGTCTCTTT 1091
Qy 979 CAGAAATCTGCTGCTG 994

Db	1092	GAGAAACACCTCTTG 1107			
RESULT 4					
CNSOABSJ					
LOCUS					
DEFINITION					
ACCESSION		CNSOABSJ		1362 bp	mRNA
VERSION					linear
KEYWORDS					HTC 06-FEB-2004
SOURCE					Arabidopsis thaliana Full-length cDNA Complete sequence from clone
ORGANISM					GSJLPGH78ZH09 of Hormone Treated Callus of strain col-0 of
REFERENCE					Arabidopsis thaliana (thale cress).
AUTHORS					
TITLE					
JOURNAL					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
gene					
ORIGIN					
Query Match					
Best Local Similarity					
Matches					
QY	79	ATTCTGTGTCGACCTACGACACCCGATGCCAAGATCTCATAGTGAACGCTGTAGG 138			
Db	192	ATCCCCGTGTCNACTTAGCCGATCCGGAAGCGAATCCGAATCTAAAGCTCGGAG 251			
QY	139	GACTTCGGCTTCTCAAGCTTGTAACCATGTTGTTCCATTGAGTTAATGGCCAAATTTA 198			
Db	252	GAGTTCGGGTCTTCAAGGTCGTAACACCGAGTCCGACCCGAACTCATGACTCGGTGA 311			
QY	199	GAAAAACGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAACAGAGCTGTCCC 258			
Db	312	GAGCAGGAGGCTATTGGCTTCTTCGGCTTGCCCTCAGTCTCTTTAAAAAACCGGCGGTCCA 371			
QY	259	CCCGACCCCTTTGGGCTATGTCAGAGAGGATTGGCCAAACGGTGATGTCGGTTGGGTC 318			
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QY	319	GAATACCTCTCTCTCAACACCAACCTGATGTTATCTCAACCCAAATCATTTCGATTTTC 378			
Db	432	GAGTATCTCTCTCTCAATGCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 491			
QY	379	CGAGAAAATCCCTCATCTATTTTCAGGGCGGTGGAGAACTACATTACACGAGTGAAGAAC 438			
Db	492	CGTCAAAACCCCTCAAAATTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 551			
QY	439	ATGTGCTATGTCGCTGTTTGAATTTGATGGCGGAGGGTTGGGGATAGAGGAGGAGGATACG 498			
Db	552	GTGTCGTACAAGGTGTTGGAGATGGTTGCCGAAGAACTAGGATAGAGCAAGGGACACT 611			
QY	499	TTAAGCAGGTTGCTGAAGATGAGAAAAGTGAATCTGCTTCAGTTGAGTTGAACCACTACCCG 558			
Db	612	CTGAGTAAATGCTGAGAGATGAGAAGTGAATCTGCTGCTGAGACTAAACCAATTTATCCG 671			
QY	559	CCTTGCCCTGAGTGCACGACTGACCGGAATTTGTTGGTGGTGGGAGGACACAGAC 618			
Db	672	GC---GGCGGAGGAGGCGGAGAGATGGTGAAGTGGGGTTTGGGAAACACACAGAC 728			
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Db	729	CCACAGATAAATCTCAGTGTCTAAGATCTAATAACCGCGGGTCTTCAAAATCTGTGTGAAA 788			
QY	679	GATGGCATTGGGTTTCACTCCACCTGATCAGACTTCTCTTTTCAATGTTTGGTGTGAC 738			
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QY	739	GCTCTACAGTAAATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 798			
Db	849	GCTCTTCAAGTAAATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 908			
QY	799	ACAAAGAAATCAAGGTTTATCAATGATCTACTTTGGAGGACCGCTGTAGTGAATAATA 858			
Db	909	ACAAGAGATCAGGATTTCAATGATATATTTTCGGCGGACCGCCATTGAGCCAGAGATC 968			
QY	859	GCACCTTACCTTCACTGATGTTAAAGAGAGAGGAGTGTGTTGACAAAAGTTCATGCG 918			
Db	969	GCACCATTCCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1028			
QY	919	TGTGAATCAAGAAGGCTCGTACACTTCAAGGCTAGCTGATATAGGCTTGGCCCTTTC 978			
Db	1029	TCTCAATAAATCTTCTGCTTCAAGTCTAAGCTTGGTGGTATATAGACTTGTGCTCTTT 1088			
QY	979	CAGAAA 984			
Db	1089	GAGAAA 1094			
RESULT 5					
CNSO9Y5Q					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
QY	79	ATTCTGTGTCGACCTACGACACCCGATGCCAAGATCTCATAGTGAACGCTGTAGG 138			
Db	192	ATCCCCGTGTCNACTTAGCCGATCCGGAAGCGAATCCGAATCTAAAGCTCGGAG 251			
QY	139	GACTTCGGCTTCTCAAGCTTGTAACCATGTTGTTCCATTGAGTTAATGGCCAAATTTA 198			
Db	252	GAGTTCGGGTCTTCAAGGTCGTAACACCGAGTCCGACCCGAACTCATGACTCGGTGA 311			
QY	199	GAAAAACGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAACAGAGCTGTCCC 258			
Db	312	GAGCAGGAGGCTATTGGCTTCTTCGGCTTGCCCTCAGTCTCTTTAAAAAACCGGCGGTCCA 371			

A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
 Unpublished
 REFERENCE 2 (bases 1 to 1141)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
 URV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
 FEATURES
 source location/Qualifiers
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 /db_xref="taxon:3702"
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 /ecotype="Col-0"
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 /gene="At1g30040"
 ORIGIN
 Query Match 42.3%; Score 421.2; DB 4; Length 1141;
 Best Local Similarity 67.3%; Pred. No. 2.5e-117;
 Matches 610; Conservative 0; Mismatches 293; Indels 3; Gaps 1;
 QY 79 ATTCTGTGTCGCTCAGCTCAGCACCCTGATGCGAAGATCTCATAGTGAACCCCTGTAGG 138
 DB 165 ATCCCGCTGTCACCTAGCCGATCCGAAGCGAAGAACCCGATCGTAAAGCCCTGCGAG 224
 QY 139 GACTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTTCCATTTGAGTTAATGCCCAATTAT 198
 DB 225 GAGTTCGGTCTTCTCAGGTCTGTAACCAAGCGAGTCCGACCGCACTCATGACTCGGTTA 284
 QY 199 GAAACGAGGCGCTCAGGTTCTTTTAAAAATCTCAGTCCGAGAAACAGAGCTGGTCCC 258
 DB 285 GAGCAGGAGGCTATTGGCTTCTTGGCTTTCCTCAGTCTCTTAAAAACCGGCGCGTCCA 344
 QY 259 CCGGACCTTCCTGCTATGTCAGAGAGATTTGCCCAACGGTGTGTCGGTGGGTC 318
 DB 345 CTGAACCGTACGGTTATGGTAATAAACGGATTTGACCAACCGGTGACGCTGGTGGATT 404
 QY 319 GAATACCTCTCTCAACCAACCTGATTTATCTCAACCAATCACTTTGCATTTTC 378
 DB 405 GAGTATCTCTCTCAATGCTATCTCTCAGCTCTCTCTCTTAAACCTCCGCGCTTTC 464
 QY 379 CGAGAAATCTCATATTTCAAGGCGGTGGTGGAGAACTCATACAGATGAAGAAC 438
 DB 465 CGTCAACCCCTCAATTTTCGCTGAGTCCGCTGGAGGATACATGAAGGAGATTAGGAA 524
 QY 439 ATGTGCTATCGGTGTGGAATTTGATGCGGAGGGGTGGGTAAGGACAGGAGATACG 498
 DB 525 GTGTGCTACAGAGTGTGGAGATGTTGCGGAGAACTAGGATGAGCAAGGACACT 584
 QY 499 TTAAGCAGGTGTGCTGAAGGATGAGAAAGTGTGCTGCTTCAAGTTGAACCACTACCG 558
 DB 585 CTGAGTAAATGCTGAGAGATGAGAGAGTACTGTGCTGAGACTAAACCATTTATCG 644
 QY 559 CTTTGCCCTGAGTGAAGCACTGAACCGGAATTTGGTTGGTTGGGAGACACAGAC 618

DB 645 GC---GGCGAGGAAGAGCGGAGAGATGCTGAAGTGGGGTTTGGGAACACACAGAC 701
 QY 619 CCACAGATAATTTCTGTCTTAAGATCTAACACACATCTGGCTTGCAAAATCTGTCTCACA 678
 DB 702 CCACAGATAATCTCAGTCTAAGATCTAATAACACGGCGGTCTTCAAATCTGTGTGAA 761
 QY 679 GATGGCACTTGGTTCAGTCCACCTGATCAGACTTCTTTTTCATCAATGTTGGTGAC 738
 DB 762 GATGAAGTTGGTGGCTGCTCCCTCCTGATCACTTCTTCTTCAATTAATGTTGGAGAT 821
 QY 739 GCTCTACAGGTAAGTAACTAAATGGGAGGTTTAAAGCTTAAAGCATAGGTTTGGCTGAC 798
 DB 822 GCTCTTACAGTTATGATTAACGGGAGGTTCAAGAGTGTAAACACAGAGGTCTTAGCCGAT 881
 QY 799 ACAACAGAGTCAAGGTTATCAATGATCTACTTTGGAGACCAAGCGTTGAGTGAATAATA 858
 DB 882 ACAAGGAGATCGAGGATTTCAATGATATATTTTCGCGGACCGCATTTGAGCGAGAATC 941
 QY 859 GCACCTTTACCTTCAGTGTATGTTAAAGGAGAGAGGTGTTGTACAAAGAGTTCACATGG 918
 DB 942 GCACCATTTGCCATGCTTGTCCCTGAGCAAGATGATTTGGCTTTACAAAGAAATTCACCT 1001
 QY 919 TGTGAATACAGAGAGGCTGCTGATCACTTCAAGGCTAGCTGATATAAGCTTCCCTTTC 978
 DB 1002 TCTCAATACAAATCTTCTGCTTACAAAGTCTAAGCTTGGTGTATAGACTTGGTCTCTTT 1061
 QY 979 CAGAAA 984
 DB 1062 GAGAAA 1067
 RESULT 6
 BUS49366/c
 LOCUS Gm-r1088 622 bp mRNA linear EST 16-SEP-2002
 DEFINITION Gm-r1088 Glycine max cDNA clone Gm-r1088-5828 3',
 mRNA sequence.
 ACCESSION BUS49366
 VERSION BUS49366.1 GI:22932227
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 622)
 Vokhin,L., Shoemaker,R., Keim,P., Retzel,E., Khanna,A., Shealy,R.,
 Clough,S., Thibaud-Nissen,F., Coryell,V., Erpelidng,J., Raph,C.,
 Shoop,E., Stromvik,M., Schweitzer,P., Gong,G. and Liu,L.
 A Functional Genomics Program for Soybean (NSF 9872565) (2002)
 Unpublished (2002)
 Other ESTs: BG881784 corresponding to Gm-c1065-2970 (5')
 Contact: Vokhin, L.O., PI, A Functional Genomics Program for
 Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional
 Genomics
 University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l-vokhin@uiuc.edu
 Insert Length: 622 Std Error: 0.00
 Plate: Gm880016A20 row: B column: 10
 Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'
 High quality sequence stop: 622.
 Location/Qualifiers
 1..622
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 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1088-5828"
 /clone_lib="Gm-r1088"
 /note="The library Gm-r1088 is a sequence-driven, reracked
 source

set of 9,216 low redundancy clones selected from cDNA libraries from various tissues and stages of development of soybean that consists of 2,706 cDNAs from germinating cotyledons (source library Gm-cl027); 1,355 cDNAs from immature seed coats (libraries Gm-cl019 and Gm-cl023); 917 cDNAs from tissue culture derived somatic embryos (source libraries Gm-cl036 and Gm-cl075); 3,275 cDNAs from germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-cl064, Gm-cl065, Gm-cl066, and Gm-cl067; and Gm-cl068); and 963 cDNAs from young leaves exposed to bacterial and fungal pathogens (source libraries Gm-cl072, Gm-cl073, and Gm-cl074). The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reackled to form library Gm-r1088 and the cDNA clones of the reackled Gm-r1088 library were then sequenced at the 3' end. The unigene selection and 3' sequencing was funded by NSF Plant Genome project #9872565 (<http://soybeanomics.croptci.uiuc.edu/>) as part of creation of a low redundancy soybean cDNA set. The source cDNA libraries were constructed by the laboratories of Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa State University, and Paul Keim, Northern Arizona University as part of the Public EST project, <http://129.186.26.94/soybeanest.html>. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, Reracking and 3' <http://web.hmc.umn.edu/biodata/nfsboy/>. The contig analysis of sequencing were conducted by services of the University of Illinois Keck Center for Comparative and Functional Genomics <http://www.biotech.uiuc.edu/keck.htm>. Note: The corresponding 5' EST from each clone in the Gm-r1088 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."

ORIGIN

Query Match 42.2%; Score 420.4; DB 5; Length 622;
Best Local Similarity 89.9%; Pred. No. 3.7e-117;
Matches 461; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 487 CAGAGGAATACGTTAGCAGGTTGCTGAAGGATGAGAAAGTCATTGCGTTCAGGTTG 546
|||||
DB 621 CAGAGGAATGCGTTGAGTGGTTGCTGAAGGATGAGAGAGATTCTTGGCTTCAGACTT 562
|||||

QY 547 AACCACTACCCGCTTGGCCCTGAGGTGCAAGCACTGAA---CCGGAATTGGTTGGGTTT 603
|||||
DB 561 AACCCNNACCGCATGCCAGAGGTGCAAGCATTGAACGGCAGAAATTGGTTGGGTTT 502
|||||

QY 604 GGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAAACAGACATCTGGCTTG 663
|||||
DB 501 GGAGAGCACACAGACCCACAGATAATTTCTGTCTTGAAGATCTAAACAGCACCTCAGGCCTG 442
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QY 664 CAAATCTGTCACAGATGCACTTGGGTTTCAGTCCACCTGATCAGACTTCTCTTTTTC 723
|||||
DB 441 CAAATCTGTCACAGATGCACTTGGGTTTCAGTCCACCTGATCAAACTTCTCTTTTTC 382
|||||

QY 724 ATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAGCAT 783
|||||

DB 381 ATCAATGTTGGTGACACTCTACAGGTGATGACTAATGGGAGGTTTAAAGTGTAAGCAT 322
|||||

QY 784 AGGTTTTGGCTGACACAACAGAGTCAAGGTTATCAATGATCTACTTTTGGAGACACAGCG 843
|||||

DB 321 AGAGTTTTGGCTGACCCCAACCAAGTCAAGGTGTGTCATGATCTACTTTTGGAGGAGCACCC 262
|||||

QY 844 TTGAGTGAATAATAGCATTACCTTCAGTCATGTTTAAAGGAGAGAGTGTGTTGTAC 903
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DB 261 TTGAGTGAATAAGATATCACCTTTACCTTCTCTCATGTTTAAAGGAGAGAGAGTGTCTAC 202
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QY 904 AAAGATTTCACATGTTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAAT 963
|||||

|||||
DB 201 AAAGAATTCCATGTTGGGAATACAGAAGGCTGGCTATGCTCAAGGCTAGCGGATAAT 142
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QY 964 AGGCTTGGCCCTTCCAGAAATCTGCTGAT 996
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DB 141 AGGCTGCTCCTTTTGAGAAATCTGCTGAT 109
|||||

RESULT 7
CNSOABKL
LOCUS
DEFINITION
CNSOABKL 1363 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPEGH20Z07 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).
BX815974
ACCESSION
VERSION
EX815974.1 GI:42471555
HTC; GSLT_cDNA.
KEYWORDS
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS
Castelli,V., Aury,J.M., Jallou,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,P., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1363)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallou O., Wincker P., Menard M., Cruaud C.,
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/banque_projet_EF/Full_length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES
Location/Qualifiers
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTPEGH20Z07"
/tissue_type="Hormone Treated Callus"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
1..1363
/gene="Atlg30040"
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Query Match 41.8%; Score 416.4; DB 4; Length 1363;
Best Local Similarity 67.0%; Pred. No. 8e-116;
Matches 607; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 79 ATTCCTGTGGTCCGCTCACGCCATCCGATGCCAAGAATCTCATAGTGAACGCTGTAG 138
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DB 193 ATCCCCGTGTCACCTAGCCGATCGGAGCGAAACCCGATCGTAAAGCGCTGCTAG 252
|||||

QY 139 GACTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTTCCATTGAGTTAATGCCAATTTA 198
|||||

DB 253 GAGTTTCGGGTTCTTCAAGGTCGTAACCAACCGAGTCCGACCCGAACTCATGACTCGGTTA 312
|||||

QY	199	GAACAGAGGCGCTCAGGTTCTTTAAATAATCTCAGTCGAGAAAGACAGAGCTGTGTCC	258
Db	313	GAGCAGAGGCTATTGGCTTCTTCGGCTTCAGTCTCTTAAATAACCGGCGGTCCA	372
QY	259	CCGAGCCCTTTCGGCTATGGTAGAGAGATTGGCCAAACGGTGATGTCTGGTGGGTC	318
Db	373	CCTGAACCGTAGGGTTATGGTAATAAAGATTGGACCAACGGTGACGTTGGTTGGATT	432
QY	319	GAATACCTCTCTCAACCAACCGCTGATTTATCTACCCCAATATCATTTGGCATTTTC	378
Db	433	TAGTATCTCTCTCAATGCTAATCTCTCAGCTCTCTCTCTTAAACCTCCGCGGTTTC	492
QY	379	CGAGAAATCTCTCATCATTTTCAGGGCGGTGGTGGAGAACTACATTACAGCATGAAGAAC	438
Db	493	CGTCAACCCCTCAAAATTTTCGGTAGTTGGTGGAGGATACATGAAGAGATTAAAGAA	552
QY	439	ATGTGCTATGCGGTGTGGAATTGATGGCGGAGGGTTGGGATATAGGAGAGGATATCG	498
Db	553	GTTCGTACAAGGTGTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCAAGGGACACT	612
QY	499	TTAAGCAGGTGCTGAAGATGAGAAAGTATCGTGTCTCAGGTTGAACCACTACCCG	558
Db	613	CTGAGTAAATGCTGAGATGAGAAAGTGACTCGTGCCTGAGACTAAACCATTTATCCG	672
QY	559	CCTTGCCCTGAGTGAAGCACTGAACCGGAATTTGGTTGGGTTTGGGAGCACACAGAC	618
Db	673	GC---GGCGAGGAGAGCGGAGAGATGGTAGGTGGGTTTGGGAGACACACAAAC	729
QY	619	CCACAGATAATTTCTCTTAAGATCTAACAGACATCTGGCTTGCMAATCTGTCTACA	678
Db	730	CCACAAATAATCTCAGTCTTAAGATCTAATAACAGCGCGGTCTTCAAATCTGTGTGAA	789
QY	679	GATGGCACTTGGTTTCAGTCCCACTGATCAGACTTCTTTTTCATCAATGTTGTGTAC	738
Db	790	GATGGAAGTTGGTGCCTGCTCCTCTGATCTCTTCTTCTTCTTCTTCTTCTTCTTCT	849
QY	739	GCTCTACAGTATGATTAATGGAGGTTTAAAGGTAAAGCATAGGCTTTGGCTGAC	798
Db	850	GCTCTTCAGTTATGATTAACGGAGGTTTCAAGAGTTTAAACAGGCTTTAGCCGAT	909
QY	799	ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACGAGTTGAGTGAAATATA	858
Db	910	ACAAGAGATCGAGGATTTCAATGATATATTTTCGGCGGACCGCAATTGAGCAGAGATC	969
QY	859	GCACCTTTACCTTCAGTGATGTTAAAGAGAGAGGAGTGTGTTACAAAAGTTACATGG	918
Db	970	GCACCAATGCGATGCTTGTCCCTGAGCAAGATGATTGGCTTTTACAAAGAAATTCATTGG	1029
QY	919	TGTGTAACAAGAGGCTCGTACACTTCAAGGCTAGCTGATATATAGGCTTGGCCCTTTC	978
Db	1030	TCTCAATAAATCTTCTGCTTACAAGCTTAAGCTTGGTGTATATAGACTTGTCTCTTT	1089
QY	979	CAGAAA 984	
Db	1090	GAGAAA 1095	
RESULT 8			
CNSOAC3R			
LOCUS			
DEFINITION			
Arabidopsis thaliana Full-length cDNA Complete sequence from clone			
thaliana (thale cress).			
Accession			
Version			
Keywords			
Source			
ORGANISM			
REFERENCE			

AUTHORS	Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1339)
AUTHORS	Genoscope.
JOURNAL	Direct Submission
TITLE	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_FF/Full-length
FEATURES	Location/Qualifiers
source	1..1339 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /clone="GSLTPB702F11" /tissue_type="Flowers and buds" /ecotype="Col-0" /plasmid="pCMVSPORT_6" 1..1339 /gene="Atlg30040"
gene	
ORIGIN	
Query Match	38.8%; Score 386.4; DB 4; Length 1339;
Best Local Similarity	66.9%; Pred. No. 1.3e-106;
Matches	581; Conservative 0; Mismatches 281; Indels 6; Gaps 2;
Qy	79 ATTCCTGTGTGACCTCAGCACCACCGATGCCAAGAATCTCATAGTGAACGCTGTAGG 138
Db	193 ATCCCCGTCTCAACCTAGCCGATCGGAAGCGAAACCCGAATCGTAAAGCCTCGGAG 252
Qy	139 GACTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCCATTTGGAGTTAATGGCAATTTA 198
Db	253 GAGTTCCGGGTTCTTCAAGGTCGTAACCAACCGAGTCCGACCGAACTCATGACTCGGTTA 312
Qy	199 GAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGTGCC 258
Db	313 GAGCAGGAGGCTATTGGCTTCTTCGGCTTGCCCTCAGTCTCTTAAAAACCGGCGGTCCA 372
Qy	259 CCGAGCCCTTTCGGCTATGTTAGCAAGATTGGCCCAACCGGTGATGTCCGTTGGGTC 318
Db	373 CCTGAACCGTACGGTTATGGTAAATAAACGATTGGACCAACCGGTGACGTTGGTTGATT 432
Qy	319 GAATACCTCTCTCAACCAACCCCTGATGTTATCTCACCCAAAATCATTTGTCATTTTC 378
Db	433 GAGTATCTCTCTCAATGCTAATCTCTCAGTCTCTCTCTCTCTTAAACCTCCGCCGTTTC 492
Qy	379 CGAGAAATCTCATCATTTTCAGGGCGGTGGTGGAGAACTACATTACAGCAGTGAAGAAC 438
Db	493 CGTCAACCCCTCAAAATTTTCGGTGAAGTCCGTGGAGGAGTACATGAAGGAGATTAAAGAA 552
Qy	439 ATGTGCTATGCGGTGTGGAATTGATGGCGGAGGGGTTGGGATATAGGAGAGGAAATACG 498
Db	553 GTGTGCTACAAGGTTGTGGAGATGGTTGCCGAAGAACTAGGATATAGAGCCAGGACACT 612
Qy	499 TTAAGCAGGTTGCTGAAGGATGAGAAAGTATTCGTGCTTTCAGGTTGAACCACTACCCG 558

Db 613 CTGAGTAATAATGCTGAGAGATGAGAAGTGAATCTGCTGCTGAGACTAAACCAATATTCG 672

Qy 559 CCTTGCCCTGAGTGAAGACACTGAACCGGAATTTGGTTGGGTTTGGGAGCACACAGAC 618

Db 673 GC---GGCGAGGAAGAGCGGAGAGATGGTGAAGTGGGGTTTGGGGAACACACAGAC 729

Qy 619 CCACAGATAATTTCTGTCTTAAGATCTACAGACACATCTGGCTTGGCAATCTGCTTCACA 678

Db 730 CCACAGATAATCTCAGTGTGAAGATCTAATAACACGCGGGCTTCAAAATCTGTGTGAA 789

Qy 679 GATGGCACTTGGGTTTCAGTCCACCTGATCAGACTTCTTTTCATCAATGTTGGTGAC 738

Db 790 GATGGAAGTTGGGTCGCTGCTCTCTGATCATCTTCTTCTCAATTAATGTTGGAGAT 849

Qy 739 GCTCTACAGTAATGACTAATGAGAGGTTTAAAGTGAAGCATAGGGTTTGGCTGAC 798

Db 850 GCTCTTTCAGTTATGACTAACGGGAGGTTCAAGAGTGTAAACACAGGGTCTTAGCCGAT 909

Qy 799 ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACACGCTGAGTGAAATATA 858

Db 910 ACAAGAGATCGAGGATTTCAATGATATATTTCCGCGGACCGCATTTGAGCCAGAAGATC 969

Qy 859 GCACCTTTACCTT---CAGTGATGTTAAAGGAGAGAGTGTGTTGACAAAGTTTACA 915

Db 970 GCACCAATGCAATGCTGCTGCTCCTCAGCAAGATGATTTGTGCTTTACAAAGAATTCAT 1029

Qy 916 TGGTGGAATACAAAGAGGCTGGGTACA 943

Db 1030 TGGTCTCAATACAAATCTTCGTTTACA 1057

RESULT 9

BE802903

LOCUS

DEFINITION

sz46c09.y1 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl051-1097 5' similar to TR:064692 064692 PUTATIVE GA4 PROTEIN.

;/ mRNA sequence.

ACCESSION

BE802903

VERSION

BE802903.1 GI:10234015

KEYWORDS

EST.

SOURCE

Glycine max (soybean)

ORGANISM

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 612)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

High quality sequence stop: 413.

FEATURES

Location/Qualifiers

1..612

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Corolla"

/db_xref="taxon:3847"

ORIGIN

Query Match 37.7%; Score 375.6; DB 2; Length 612;

Best Local Similarity 88.3%; Pred. No. 2.1e-103;

Matches 408; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 1 ATGGTTGTTCTGCTCAGCCAGCATTAACCAAGTTTTCCTCTGAAACCATTCAGATCC 60

Db 151 ATGGTTGTTCTGCTCAGCCAGCATTAACCAAGTTTTCCTCTGAAACCATTCAGATCC 210

Qy 61 ACGCCCTTCTTCCACGGGGATTCCTGTGGTCGACCTCACGACCCCGATGCCAAGATCTC 120

Db 211 ACGCCCTTCTTCCACGGGGATTCCTGTGGTCGACCTCACGACCCCGATGCCAAGATCTC 270

Qy 121 ATAGTGAACGCTGTAGGGACTTCGGCTTCTTCAAGCTTTGTGAACCATTCGTTCCATTG 180

Db 271 ATAGTCAATGCTGTAGGGACTTCGGCTTCTTCAAGCTTTGTGAACCATTCGTTCCATTG 330

Qy 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGTTCTTTTAAATAATCTCAGTCCGAG 240

Db 331 CAGTTTCATGGCCAAATTTGGAAAACGAAACCTCGGGTCTTCAAAAACCTCAATCCGAG 390

Qy 241 AAAGACAGAGCTGCTCCCGCCGACCTTTCGGCTATGGTAGCAAGAGGATTCGCCCAAC 300

Db 391 AAAGACAGAGCTGCTCCCGCCGACCTTTCGGCTATGGTAGCAAGAGGATTCGCCCAAC 450

Qy 301 GGTGATGTCGGTTGGTTCGAATACCTCTCTCAACACCAACCTGATTTATCTCACCC 360

Db 451 GCGGATGTCGGTTGGTTCGAATACCTCTCTCAACACCAACCTGATTTATCTCCCC 510

Qy 361 AAATCAGCTTTCGATTTTCGAGAAAATCTCATCATTTTCAGGCGGTGTGGAGAACTAC 420

Db 511 AAGTCACAGTTTCATTTTCAGAGAACGTCCTCAGAATTTTCATGCGGTGTGGAGGAATAC 570

Qy 421 ATTACAGCAGTCAAGAACATGCTATGCGGTGTTGGAAATTG 462

Db 571 ATTAGAGCGGTGAACACATGTCTATGACGTGGTGGAAATTG 612

RESULT 10

AJ803092

LOCUS

DEFINITION

Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018 5_05_018, mRNA sequence.

ACCESSION

AJ803092

VERSION

AJ803092.1 GI:51118420

KEYWORDS

Antirrhinum majus (snapdragon)

SOURCE

Antirrhinum majus

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.

REFERENCE

1 (bases 1 to 785)

Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H., Siedler, H. and Zachgo, S.

Characterization of Antirrhinum Petal Development and

/clone="GENOME SYSTEMS CLONE ID: Gm-cl051-1097"

/tissue_type="floral meristematic mRNA"

/lab_host="DH10B"

/clone_lib="Gm-cl051"

/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

Identification of Target Genes of the Class B MADS Box Gene										
JOURNAL	DFICIENS	Plant Cell 16 (12), 3197-3215 (2004)	15539471	Contact: Schwarz-Sommer Z	Molekulare Pflanzen-genetik	MPI fuer Zuechtungs-forschung	Carl-von-Linne Weg 10, D-50829, Germany.	Location/Qualifiers	source	
COMMENT										
FEATURES	1. .785 /organism="Antirrhinum majus" /mol_type="mRNA" /db_xref="taxon:4151" /clone="018_5_05_018" /tissue_type="whole plant" /clone_lib="Antirrhinum majus whole plant"									
ORIGIN										
Query Match	35.7%;	Score 355.8;	DB 1;	Length 785;						
Best Local Similarity	68.4%;	Pred. No. 2.7e-97;								
Matches 508;	Conservative 0;	Mismatches 232;	Indels 3;	Gaps 1;						
Qy	235	TCGAGAAAGACAGACGTGGTCCCCCGACCCCTTTCCGCTATGTCACAGAGGATTGGC	294							
Db	20	TCGTAAAGAGAGAAAACAGGGGACCCCTGACCCCTTTGGCTATGGAAGTAAGAAAAATTTGGA	79							
Qy	295	CCAAACCGGTGATGTGCGGTGGGTGCAATACCTCTCTCTCAACCAACCCCTGATGTTATC	354							
Db	80	CGCAATGGCGATGGGATGGTTCGATATCTTGTCTCTTAACACTAATCTGATCTCTGAT	139							
Qy	355	TCACCCAAATCATTGTCATTTTCCGAGAAAATCCTCATCATTTTCAGGCGGGTGGTGAG	414							
Db	140	TACAGAAAAATTTGCATCGGTTTTTTGGTGAAGCTGCAGAAAAAATTCAGGTGTATAGTGAAT	199							
Qy	415	AATCTACATTACAGCAGTGAAGACATGTCTATCGGTGTGGGAATTCATGCGCGGAGGGG	474							
Db	200	GATTATGTTTCTGCAGTAAAGAGAAATGGCGTGCAGATTCCTTGAATAATGTTGGCTGATGAA	259							
Qy	475	TTGGGGATAAGCGACAGAGAAATACCTTAAAGCAGGTTGCTGAAGGATGAGAAAATGATTTCG	534							
Db	260	CTTAAGATTCAACAAAGGACCGCTTTTAGCBAACCTTTTATGGATGAACAGAGTGACTCT	319							
Qy	535	TGCTTCAGGTTGAACCACTACCCGCTTGCCCTGAGGTGAAGCACTGAACCGGAATTTTG	594							
Db	320	GTTTTCAGGCTAAATCACTATCCACCATGCCCGAAATTTCAAGAATCCAAC---AACTTA	376							
Qy	595	GTTCGGTTTGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTTAACAGACACA	654							
Db	377	ATCGGGTTTGGTGAACATACTGACCCCGCAATAATATATCCGTTTTTGAGATCCAAACAAC	436							
Qy	655	TCCTGGCTTGCAAAATCTGTCTCACAGATGGCACTTTGGGTTTCAGTCCCAACCTGATCAGACT	714							
Db	437	TCGGGTCTTCAAAATTTGTTGAAGATGGGAATTTGGAATTTCTATCCCACTGATCAAGT	496							
Qy	715	TCCTTTTTCATCAATGTTGGTGAAGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGT	774							
Db	497	TCCTTCTTCATTAATGTTGGTGAAGCTCACTGCAGGTTATGACTAATATGGCAGGTTTAAAGT	556							
Qy	775	GTAAGACATAGGGTTTTGGCTGACACACAGAGTCAAGGTTATCAATGATCTACTTTGGA	834							
Db	557	GTAAGACACAGGGTTTGGCCCAACAGCTCAAAACCAAGACTTTTCAATGATATATTTTTGGA	616							
Qy	835	GGACACGGTTGAGTGAATAATATAGCACTTTTACCTTCAGTGATGTTTAAAGAGAGAGAG	894							
Db	617	GGACCAACATTAAGTGAAGAGATAGCTCCATTTGCTTCAGTACTAATGAAGAGGAGAGAC	676							
Qy	895	TGTTTGTACAAGAGTTTCAATGGTGTGAATACAAAGAGGCTCGGTACCTTCAAGGCTA	954							
Db	677	AGCTTGTACAAGGAATTTACTTTGGTTTGAGTACAAAAAATCTGCTTATATCAAGGCTGG	736							
Qy	955	GCTGATTAATAGGCTTGGCCCTTTT	977							
Db	737	GCTGATTAATAGGCTGCTGTTT	759							

Db 264 CCACAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAGAATGGTTCGGAATGGTG 320
QY 305 ATGTCGGTTGGGTCGAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCCCAAT 364
Db 321 ACGTGGGTTGGGTTGAGTACTTGTGATGAACGCTAATCATGATTCGGGTTCCGCTCCAC 380
QY 365 CACTTTGCAATTTCCGAGAAATCCCTCATCTTTCAGGGCGGTGGGAGAACTACATTA 424
Db 381 TATTTCCAGTCTTCTCAAAAGCCCGGGAACCTTTCAGAAACGCAATTTGGAAGAGTACAAA 440
QY 425 CAGCAGTGAAGAACATGTCTGATGCGGTGTGGAATTTGATGGCGGAGGGTTGGGGATAA 484
Db 441 CATCAGTGAGAAAATGACATTCGATGTTTGGAGAGATCACAGATGGCTAGGGATCA 500
QY 485 GGAGAGGAATAGCTTAAAGCAGGTGCTGAAGATGAGAAAGTGAATTCGTGCTTCAGGT 544
Db 501 AACCGAGGAACACACTTAGCAAGCTTGTATCTGACCAAAACACGGACTCGATATTGAGAC 560
QY 545 TGAACCACTACCGCCTTCGCTGAGGTGCAAGCACTGAAC-----CGGAATTTGG 595
Db 561 TTAATCAGTATCCACCATGTCCTTTAGCAATGAAGAAACCAATGGTGAAGATGTGA 620
QY 596 TTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAACAGACAT 655
Db 621 TTGGTTTGGTGAACACACAGATCCTCAATCATTTCTGTCTTAAAGATCTAACACACTT 680
QY 656 CTGGCTTGCAATCTGCTCACAGATGGCATTTGGGTTTCAGTCCCACTGATCAGACTT 715
Db 681 CTGGTCTCAAAATTAATCTAAATGATGGCTCATGGATCTCTGTCCCTCCGATCAGACTT 740
QY 716 CTTTTTTCAATGTTGGTGACGCTCACAGTAATGACTAATGGAGGTTTAAAGTG 775
Db 741 CCTTCTCTTCAACGTTGGTGACTCTCCAGGTGATGACAAATGGAGGTTCAAGAGCG 800
QY 776 TAAAGCATAGGGTTTGGGTGACACAAACGAAGTCAAGGTTTATCAATGATCTACTTTGGAG 835
Db 801 TGAGGCATAGGGTTTGTAGTCACTGTGAAAAATCTAGGGTTTCTATCATTTACTTCGCTG 860
QY 836 GACCAGCGTTAGTGAATAATAGCACTTTTACCTTCAGTGATGTTTAAAGAGAGAGGT 895
Db 861 GACCTTCATTTGACTCAGAGAAATCGCTCCGTTTCAATGTTTATGATAGCAATGAGAGCAGA 920
QY 896 GTTTGTACAAAGATTCACATGTGTGTAATACAGAGGCTGGTACACTTCAAGGCTAG 955
Db 921 GGTGTACAGAGGATTTACTTGTGCTGTAATACAAAACTCTACTACAACCTTAGATTGT 980
QY 956 CTGATAATAGGCTTGCCCTTTCCAGA 982
Db 981 CTGATAATAGGCTTCAACAATTCGMA 1007

RESULT 12
BI208568
LOCUS 694 bp mRNA linear EST 11-JUL-2001
DEFINITION EST526608 cTOS Lycopersicon esculentum cDNA clone cTOS17020 5' end,
mRNA sequence.
ACCESSION BI208568
VERSION 1 GI:14686292
KEYWORDS EST.
SOURCE Lycopersicon esculentum (solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 694)
REFERENCE van der Hoeven,R., Sun,H., Bezzerides,J., Cho,J., Utterback,R.,
Ronning,C. and Tanksley,S.
Generation of ESTs from Tomato Suspension Cultures
Unpublished (2001)
CONTACT: CUGI
Clemson University
Clemson University
Clemson University

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES
source
1..694
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496, E6203"
/db_xref="taxon:4081"
/clone="cTOS17020"
/tissue_type="suspension cultures"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).
Fresh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
shaking."

ORIGIN

Query Match 33.7%; Score 335.4; DB 2; Length 694;
Best Local Similarity 69.6%; Pred. No. 4.8e-91;
Matches 485; Conservative 0; Mismatches 206; Indels 6; Gaps 2;
QY 269 TCGGCTATGCTAGCAGAGGATTGGCCCAACGGTGATCGGTTGGGTGCGAATACCTCC 328
Db 1 TTGGTTATGGCAATAGAAAAATCGGACAAAATGGCGATATCGGTTGGGTTGAATACATTC 60
QY 329 TCTCAACACCAACCCCTGATGTATCTCACCAAAATCACTTTTGCAATTTTCCGAGAAAATC 388
Db 61 TCTTTTCACAAAATCTGAAATTCNATTACCAGAAATTCGCACTGTATTAGGTGTCATC 120
QY 389 CTCATCATTTACGGCGGTGGTGGAACTACATTACAGAGTGAAGACATGTGCTATG 448
Db 121 CAGMAAACATTCGGGTCGGGTGAATGATATGTGTCTCATCAGTGAAGAAAAATGTCATGTG 180
QY 449 CGGTGTTGAAATGATGGCGGAGGGTTGGGATAAGGCAGAGGATACGTTAAGCAGGT 508
Db 181 AGATTCTTGAAGAATTTGGCGGAGGGATTAAAGATTCAACCGACGAATGTTTGAAGTAAGC 240
QY 509 TGTGAAGGATCAGAAAAAGTGAATTCGTGCTTCAGGTTGAACCACTACCGCCCTTGCCTTG 568
Db 241 TATTGATGATGAAGAGCGACTCTGTTTTCAGGCTGAATCACTATCTCCATGCTCTG 300
QY 569 AGGTCAAGACACTGAA---CCGGAATTTGGTGGGTTTGGGGAGCACAGACCCACAGA 625
Db 301 ATATTCAAGAAATTCATGCGCAAAAATTTAATTTGGATTGGAGAACATACCTGATCCCAA 360
QY 626 TAAATTTCTGCTTAAGATCTAACAGCACATCTGGCTTGCANAATCTCTCACAGATGGCA 685
Db 361 TCATGTCGATTTTAAGATCAACACACTTCGCGTCTTCAAAATTTTACTCAAAAATGGCA 420
QY 686 CTTGGGTTTCAGTCCCAACCTGATCAGACTTCCTTTTTCATCAATGTTGTGAGCGCTTAC 745
Db 421 ACTGGTTTCTGTTCATCTGATCAGAAATCTTTTTTCGTCATGTTGGAGACTCATTAC 480
QY 746 AGGTAAATGACTAATGGAGGTTTAAAGTGAAGCATAGGGTTTGGGTGACACACAGA 805
Db 481 AGGTGATGACGAATGGAAGTTTAAAGATGTGAAAACATAGGGTGTTCACAAACAGTGTGA 540
QY 806 AGTCAGGTTATCAATGATCTACTTTTGGAGGACCGGTTGAGTGAATAATATAGCACCTT 865
Db 541 AATCAAGACTATCAATGATATATTTTGGAGGACCCATTCATGAGTGAAGATAGCACCAT 600
QY 866 TACCTTTCACTGATGTTTAAAGAGGAGGAGTGTGTTGTACAAAGAGTTTCACATGCTGTGAAT 925
Db 601 TGGCATCACTAATG---GAAGGGAAGACAGTTTATACAAAGAGTTTACATGCTTTCAGT 657
QY 926 ACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAA 962
Db 658 ACCAAAAGTCAGCTTACAAGACTAGACTAGCTGATAA 694


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RESULT 13
BM893076
LOCUS
DEFINITION
    BM893076 567 bp mRNA linear EST 05-JUL-2004
    sam51f05.v1 Gm-cl069 Glycine max cDNA clone SOYBEAN CLONE ID:
    Gm-cl069-2961 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA
    sequence.
ACCESSION
BM893076.1 GI:19348544
VERSION
BM893076.1
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 567)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
FEATURES
    source
        1. 567
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            /mol_type="mRNA"
            /cultivar="Williams"
            /db_xref="taxon:3847"
            /clone="SOYBEAN CLONE ID: Gm-cl069-2961"
            /tissue type="degenerating cotyledons, 9-10 day old
            etiolated seedling"
            /lab host="DH10B"
            /clone lib="Gm-cl069"
            /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
            XhoI; The cDNA library was constructed from mRNA isolated
            from degenerating cotyledons of 9-10 day old etiolated
            seedlings for the cultivar Williams. Complementary DNA was
            synthesized from mRNA using a primer consisting of a
            poly(dT) sequence with a XhoI restriction site. EcoRI
            adapters were ligated to the blunt-ended cDNA fragments
            followed by XhoI digestion. The cDNA fragments were
            directionally cloned into the EcoRI-XhoI restriction site
            of the pBluescript vector. The ligated cDNA fragments
            were transformed into DH10B host cells (GibcoBRL). This
            library was constructed in the laboratory of Dr. Randy
            Shoemaker."
ORIGIN
Query Match 33.6%; Score 334.8; DB 3; Length 567;
Best Local Similarity 88.5%; Pred. No. 6.9e-91;
Matches 363; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 ATGGTGTCTCTCAGCCAGCATGAACCAAGTTTTCCTCTCGAACCATTCAAGTCC 60
DB 157 ATGGTGTGTTTGTCTCAGCCAGCATTAACCAAGTTTTCCTCTCTGAAAAACATGCAAGCC 216

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QY 61 ACGCCCTTGTTCACGGGGATTCTCTGTGTCGACCTCAGCACCACCGGATGCCAAGATCTC 120
DB 217 ACGCCCTTGTTCACGGGGATTCTCTGTGTCGACCTCAGCACCACCGGATGCCAAGATCTC 276
QY 121 ATAGTGAACGCTCTAGGAGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 180
DB 277 ATAGTGAAGGCTGACGGGACTTTCGGCTTCTTCAAGCTCTGTGACCAAGGATGTTCCATTA 336
QY 181 GAGTTAATGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAG 240
DB 337 GAGTTAATGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAG 396
QY 241 AAAGACAGAGCTGTGTCCTCCCGACCCCTTCGCTATGCTAGCAGAGAGATTGGCCCAAC 300
DB 397 AAAGACAGAGCTGTGTCCTCCCGACCCCTTCGCTATGCTAGCAGAGAGATTGGCCCAAC 456
QY 301 GGTGATGTGGTTCGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACC 360
DB 457 GGTGATGTGGTTCGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACC 516
QY 361 AAATCATTTCATTTTCCGAGAAAAATCTCATCATTTTCAGGGCGGTGGT 410
DB 517 AAGTCACAGTTTCATTTTCCGAGAAAAATCTCATCATTTTCAGGGCGGTGGT 566

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RESULT 14
AL382874
LOCUS
DEFINITION
    AL382874 478 bp mRNA linear EST 03-AUG-2000
    MtBC10E02F1 MtBC Medicago truncatula cDNA clone MtBC10E02 T3, mRNA
    sequence.
ACCESSION
AL382874
VERSION
AL382874.1 GI:9682625
KEYWORDS
EST.
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 478)
Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
Niebel,A., Carreau,V., Chatagnier,O., Kahn,D.,
Gianinazzi-Pearson,V. and Gamas,P.
Medicago truncatula ESTs from endomycorrhizal roots
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
FEATURES
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        1. 478
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            /mol_type="mRNA"
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            /clone="MtBC10E02"
            /tissue type="arbuscular mycorrhiza"
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            intraradices"
            /clone lib="MtBC"
            /note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
            XhoI; M. truncatula sterilised seeds were germinated for
            72h at 25 C, before transplanting into a 1/3 Epioisses soil
            : 2/3 calcined Terragreen mix in the presence of onion
            root fragments colonized by the arbuscular mycorrhizal
            fungus Glomus intraradices (Schenck & Smith, isolate
            LPAB). The plants were watered every day and twice a week
            with a modified nutrient Long Ashton solution without

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phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of fungal origin."

ORIGIN

Query Match 33.4%; Score 332.8; DB 1; Length 478;
Best Local Similarity 83.0%; Pred. No. 2.7e-90;
Matches 395; Conservative 0; Mismatches 72; Indels 9; Gaps 1;

QY 490 AGAATACCTTAAGCAGGTTCGTGAAGGATGAGAAAGTGATCGTCTTCAGGTGAAC 549
|||||
Db 3 AAGAAATGCTTAAGCAGGTTATTGAAGATGAGAAAGTGATCTTGTTCAAAATTAAC 62
|||||

QY 550 CACTACCCGCTTGCCTGAGTGCAGCA-----CTGAACCGGAATTTGTTGGG 600
|||||
Db 63 CATTACCCACCGCTGAGTGCAGCAAGCAGCAATGAATGGAAGGAATTTGCTTGGG 122
|||||

QY 601 TTTGGGGAGCACAGACCCACAGATAATTTCTGTCTTAAGATCTAAACAGCACATCTGGC 660
|||||

Db 123 TTTGGGAGCATACAGACCCACAGTCATTTCTGCTTGAGATCTAATAGCACATCAAGA 182
|||||

QY 661 TTGCAAACTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTT 720
|||||

Db 183 CTGCAAACTGTCTCAGTGAACCTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTT 242
|||||

QY 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGAAG 780
|||||

Db 243 TTCATCAATGTTGGTGATATCTCTCAGGTAATGACTAATGGGAGGTTTAAAGTGAAG 302
|||||

QY 781 CATAGGTTTTGGCTGACACAAGAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCA 840
|||||

Db 303 CATAGGTTTTGGCTGACACAAGTCAAGGTTGCTGATGATATCTTTGGAGGACCA 362
|||||

QY 841 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGAATTTAAAGGAGAGGAGTGTG 900
|||||

Db 363 CCCTTGAGTGAAGAAGATAGTGCTTTACCTTCTTTAATGTTAAAGAAAGAAAGTTTG 422
|||||

QY 901 TACAAAGCTTTCACATGGTGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGC 956
|||||

Db 423 TACAAAGAGTTTCACTGCTTGGAGTACAAAGAACCAATGTACAATTTCAAGGCTGGC 478
|||||

RESULT 15

DN589159 893 bp mRNA linear EST 15-MAR-2005
LOCUS 50141.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
50141 5', mRNA sequence.

ACCESSION DN589159

VERSION DN589159.1 GI:61239615

KEYWORDS EST.

SOURCE Solanum tuberosum (potato)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 893)

Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Legge, M., De
Koeber, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)

Contact: Barry Flinn

The Canadian Potato Genome Project - BioAtlantech

921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA

Email: bflinn@bioatlantech.nb.ca

Seq primer: T3.

FEATURES
source

Location/Qualifiers
1..893
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="50141"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/clone_lib="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Query Match 33.1%; Score 329.2; DB 8; Length 893;
Best Local Similarity 67.6%; Pred. No. 4.2e-89;
Matches 495; Conservative 0; Mismatches 228; Indels 9; Gaps 2;

QY 262 GACCTTTTGGCTATGGTAGCAAGAGGATTTGCCAAACGGTGATGTGGTTGGGTGAA 321
Db 3 GACCTTTTGGCTATGGAAATAAGAAATTTGACCTAATGGTGTATGGTTGGGTGAA 62
|||||

QY 322 FACCTCTCTCTCAACCAACCCCTGATGTATCTCACCCCAATCACTTTGCAATTTCCGA 381
|||||

Db 63 TACATTTCTTTTGTCAACAAATTTCTGAGTTCAATTACCAGAAATTTGCATCTATTTGGGT 122
|||||

QY 382 GAAAACTCTCATCTTTTCAAGGCGGTGGTGAGAACTACATTTACAGCAGTGAAGAACATG 441
|||||

Db 123 GTCAATCCAAAGATATAAGAGATCTGTGATGATTATGATTAGCAATGAAGAAATG 182
|||||

QY 442 TGCTATGCGGTGTTGGAATTTGATGGCGAGGGTTGGGGATAAGGCAGAGGAATACGTTA 501
Db 183 GCTTGTGAGATCTTTGAAATGTTAGCAGAGGGATTTAAATAATTCATCCAAAGAAATGTATTT 242
|||||

QY 502 AGCAGGTTGCTGAAGGATCAGAAAGATGATTCGTCTTCAGCTTGACCACTACCGCCT 561
Db 243 AGTAAGCTTTTAAATGGATGAAAAAAGTGAATTCATTTTAGGCTAATCATTTACCCCTCA 302
|||||

QY 562 TGCCCTGAGG-----TGCAAGCACTGAACCCGGAATTTGGTTGGGTTTGGGGAGCACACA 615
Db 303 TGCTCTGATGATTTTCAAGATATATATGAAGAAATTTAATTTGGATTGGTGAACATCT 362
|||||

QY 616 GACCACAGATAAATTTCTGTCTTAAGATCTAACACACATCTGGGTGCAAAATCTGTCTC 675
Db 363 GATCCACAAATTTATTTCTTTTAAAGATCCAATAACACTTCTGGACTTCAAAATTTCACTT 422
|||||

QY 676 ACAGATGGCACTTGGTTCAGTCCCACTGATCAGACTTCTTTTTCATCAATGTTGGT 735
Db 423 GTTGTGTCATTTGGAATTTCTGTCCACCTGATCAAAATTTCAATTTCTTCATCAATGTTGT 482
|||||

QY 736 GACGCTCTACAGGTAATGACTAATGGAGGTTTAAAGTGAAGCATAGGGTTTGGCT 795
Db 483 GATTCAATTCAGGATGATGACAAATGGAGGTTTAAAGATGAAGATAGAGTTTGGCC 542
|||||

QY 796 GACACAAAGAACTCAAGGTTATCAATGATCTACTTTGGAGGACCGCGTTGAGTGAATAAT 855
Db 543 AATAGTGTAAAAATCAAGACTCTCAATGATTTATTTTGGAGGGCCACCATTTGAGTGAAGAAG 602
|||||

QY 856 ATAGCACCTTTTACCTTCACTGATGTTTAAAGAG---AGGAGTGTGTTACAAAGAGTTC 912
Db 603 ATAGCACCAATTTGTCATCACTATTATAAAGGGGATCAAGACAGCTTTGTACAAAGAAATTT 662
|||||

Qy	913	ACATGGTGTGAATACAAGAAGGCTGGGTACACTTCAAGGCTAGCTGATAAATAGGCTTGCC	972
Db	663	ACATGGTTTGAGTACAAAAATTTCAGCATATAAATCTAGATTGGCTGATAAATAGGTTGGTC	722
Qy	973	CCTTTCAGAA	984
Db	723	CTATTGAGAA	734

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 17:48:03 ; Search time 202.729 Seconds
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Searched: 1303057 seqs, 888780828 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	100.0	1318	3	US-09-719-108-1
2	827.4	83.1	1359	3	US-09-371-307-62
3	424.4	42.6	1237	3	US-09-719-108-7
4	421.4	42.3	1352	3	US-09-614-912-13
5	419.8	42.1	1365	3	US-09-614-912-5
6	418.2	42.0	1403	3	US-09-371-307-64
7	381.6	38.3	1008	3	US-09-719-108-9
8	362.6	36.4	1473	3	US-09-614-912-7
9	356.6	35.8	1318	3	US-09-719-108-5
10	354	35.5	1650	3	US-09-614-912-3
11	314.2	31.5	1555	3	US-09-614-912-1
12	307.8	30.9	783	3	US-09-371-307-67
13	166	16.7	811	3	US-09-371-307-71
14	155.6	15.6	403	3	US-09-371-307-66
15	154.8	15.5	406	3	US-09-371-307-68
16	152.4	15.3	966	3	US-09-371-307-58
17	120	12.0	426	3	US-09-371-307-70
18	112	11.2	450	3	US-09-614-912-3
19	103	10.3	210	3	US-09-719-108-3
20	101	10.1	199	3	US-09-719-108-4
21	79	7.9	595	3	US-09-614-912-15
22	75.8	7.6	618	3	US-09-614-912-11
23	72.4	7.3	723	3	US-09-371-307-56
24	72.4	7.3	4170	3	US-09-371-307-57

25	71.8	7.2	1228	2	US-08-823-986A-1	Sequence 1, Appli
26	71.8	7.2	1228	3	US-08-784-385-1	Sequence 1, Appli
27	71.8	7.2	1270	6	PCT-US95-10403-1	Sequence 1, Appli
28	71.8	7.2	1663	2	US-08-823-986A-3	Sequence 3, Appli
29	71.8	7.2	1663	3	US-08-784-385-3	Sequence 3, Appli
30	71.8	7.2	1703	6	PCT-US95-10403-3	Sequence 3, Appli
31	69	6.9	810	3	US-09-371-307-60	Sequence 60, Appli
32	68.6	6.9	376	3	US-09-371-307-69	Sequence 69, Appli
33	60	6.0	1030	3	US-09-371-307-5	Sequence 5, Appli
34	56.4	5.7	1017	3	US-10-155-435-5	Sequence 5, Appli
35	54.4	5.5	976	3	US-08-793-666-2	Sequence 2, Appli
36	54.4	5.5	992	3	US-08-793-666-12	Sequence 12, Appli
37	54.4	5.5	995	3	US-08-793-666-13	Sequence 13, Appli
38	54.2	5.4	1275	3	US-08-793-666-9	Sequence 9, Appli
39	54	5.4	1320	2	US-08-695-412B-13	Sequence 13, Appli
40	54	5.4	1320	3	US-09-255-154D-13	Sequence 13, Appli
41	54	5.4	1320	3	US-10-213-452A-13	Sequence 13, Appli
42	53.8	5.4	634	3	US-09-614-912-41	Sequence 41, Appli
43	51.6	5.2	1230	3	US-08-793-666-14	Sequence 14, Appli
44	50	5.0	1066	3	US-09-614-912-43	Sequence 43, Appli
45	49.8	5.0	1291	3	US-08-555-755C-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-719-108-1
; Sequence 1, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-09-719-108-1

Query Match 100.0%; Score 996; DB 3; Length 1318;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGTTGTTCTCTCTCAGCCAGCATTTGAACCAAGTTTTCTTCTCTGAAACCAATTCAGTCC	60
DB	68	ATGGTTGTTCTCTCTCAGCCAGCATTTGAACCAAGTTTTCTTCTGAAACCAATTCAGTCC	127
QY	61	ACGCCCTTTGTTTCAGGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAAGATCTC	120
DB	128	ACGCCCTTTGTTTCAGGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAAGATCTC	187
QY	121	ATAGTGAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTTCCATTG	180
DB	188	ATAGTGAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTTCCATTG	247
QY	181	GAGTTAATGGCCAAATTTAGAAAACGAGCCCTCAGTCTTTTAAAAAATCTCAGTCCGAG	240
DB	248	GAGTTAATGGCCAAATTTAGAAAACGAGCCCTCAGTCTTTTAAAAAATCTCAGTCCGAG	307
QY	241	AAAGACAGAGCTGGTCCCGCCGACCCCTTTCGGCTATGTGACGAGGATTGGCCCAAC	300

Db 308 AAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGGTAGCAAGAGGATTTGSCCCAAAC 367
Qy 301 GGTGATGTCGGTGGGTGCAATACCTCTCTCTCAACACCAACCTGATGTTATCTCACCC 360
Db 368 GGTGATGTCGGTGGGTGCAATACCTCTCTCAACACCAACCTGATGTTATCTCACCC 427
Qy 361 AAATCACTTTGCAATTTCCGAGAAATCCTCATCATTTTCAGGCGGCTGGTGAGAACTAC 420
Db 428 AAATCACTTTGCAATTTCCGAGAAATCCTCATCATTTTCAGGCGGCTGGTGAGAACTAC 487
Qy 421 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAATTTGATGCGAGGGTTGGGG 480
Db 488 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAATTTGATGCGAGGGTTGGGG 547
Qy 481 ATAAAGCAGAGGATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGAATCGTGTTC 540
Db 548 ATAAAGCAGAGGATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGAATCGTGTTC 607
Qy 541 AGGTTGAAACACCTACCCGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGG 600
Db 608 AGGTTGAAACACCTACCCGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGG 667
Qy 601 TTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGCG 660
Db 668 TTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGCG 727
Qy 661 TTGCAATCTGTCTACAGATGSCACTTGGGTTTCAGTCCACCTGATCAGACTTCCCTTT 720
Db 728 TTGCAATCTGTCTACAGATGSCACTTGGGTTTCAGTCCACCTGATCAGACTTCCCTTT 787
Qy 721 TTCAATCAATGTTGGTCAAGCTCTACAGGTAAATGACTAAATGGGAGGTTTAAAGTGTAAG 780
Db 788 TTCAATCAATGTTGGTCAAGCTCTACAGGTAAATGACTAAATGGGAGGTTTAAAGTGTAAG 847
Qy 781 CATAGGGTTTGGCTGACACCAACGAAGTCAAGGTTTCAATGATCTACTTTTGGAGGACCA 840
Db 848 CATAGGGTTTGGCTGACACCAACGAAGTCAAGGTTTCAATGATCTACTTTTGGAGGACCA 907
Qy 841 GCGTTAGTGAAATATAGCACCTTTACCTTCAGTATGATTTAAAGGAGAGGATGTTTG 900
Db 908 GCGTTAGTGAAATATAGCACCTTTACCTTCAGTATGATTTAAAGGAGAGGATGTTTG 967
Qy 901 TACAAAGAGTTTCAATGGTGTGAATACAAAGAGGCTGCGTACACTTTCAAGGCTAGCTGAT 960
Db 968 TACAAAGAGTTTCAATGGTGTGAATACAAAGAGGCTGCGTACACTTTCAAGGCTAGCTGAT 1027
Qy 961 AATAGGCTTGCCCTTTCCAGAAATCTGCTGTGAT 996
Db 1028 AATAGGCTTGCCCTTTCCAGAAATCTGCTGTGAT 1063

RESULT 2

US-09-371-307-62
; Sequence 62, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62

; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-307-62

Query Match 83.1%; Score 827.4; DB 3; Length 1359;
Best Local Similarity 89.9%; Pred. No. 3.5e-268;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;

Qy 1 ATGGTGTGTTCTCTCTCAGCCAGCATTTGAACCAAGTCTTCTTCTGAAACCATTTCAAGTCC 60
Db 102 ATGGTGTGTTCTCTCTCAGCCAGCATTTAAACCAAGTCTTCTTCTGAAACCATTTCAAGTCC 161
Qy 61 AGCCCTCTGTTTCAACGGGGATTCCTGTGGTTCGACCTCAACGACCCCGGATGCCAAGAACTCTC 120
Db 162 AGCCCTCTGTTTCAACGGGGATTCCTGTGGTTCGACCTCAACGACCCCGGATGCCAAGAACTCTC 221
Qy 121 ATAGTGAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCAATG 180
Db 222 ATAGTGAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCAATG 281
Qy 181 GAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAG 240
Db 282 CAGTTTCATGGCCCAATTTGGAAAACGAAACCCCTCGGGTTCTTCAAAAACCTCAATCCGAG 341
Qy 241 AAAGACAGAGCTGGTCCCGCCGACCTTTTCGGCTATGGTAGCAAGAGGATTTGGCCCAAAAC 300
Db 342 AAAGACAGAGCTGGTCCCGCCGACCTTTTCGGCTATGGTAGCAAGAGGATTTGGCCCAAAAC 401
Qy 301 GGTGATGTCGGTGGGTGCAATACCTCTCTCAACACCAACCTGATGTTATCTCACCC 360
Db 402 GCGGATGTCGGTGGGTGCAATACCTCTCTCAACACCAACCTGATGTTATCTCACCC 461
Qy 361 AAATCACTTTGCAATTTCCGAGAAATCTCTCATCATTTTCAGGGCGGTGGTGAGACTAC 420
Db 462 AAGTCACAGTTCATTTTCAGAGAAGGTCCTCAGAAATTTTCAGGGCGGTGGTGAGGAATAC 521
Qy 421 ATTACAGCAGTGAAGAAACATGTGCTATGGGTGTTGGAAATTCATGGCGGAGGGTTGGGG 480
Db 522 ATTACAGCAGTGAAGAAACATGTGCTATGAGGTGTTGGAAATTCATGGCTGAGGGATGGGG 581
Qy 481 ATAAAGCAGAGGAAATCGTTAAGCAGGTTGCTGAAGGATGAAGAAAGTGAATGCTGCTTC 540
Db 582 ATAAAGCAGAGGAAATCGTTAAGCAGGTTGCTGAAGGATGAAGAAAGTGAATGCTGCTTC 641
Qy 541 AGGTTGAACCACTACCCGCTTTCGCTGAGGTGCAAGCACTGAC--CGGAATTTGGTT 597
Db 642 AGACTTAAACCACTACCCGCTTTCGCTGAGGTGCAAGCAATTTGAACGGAAGGAATTTGGTT 701
Qy 598 GGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTTAACAGCACATCT 657
Db 702 GGAATTTGGAGACACACAGACCCACAGATAATTTCTGCTTCTGAGATCTTAACAGCACCTCA 761
Qy 658 GCGTTGCAAACTGTCTCAACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTC 717
Db 762 GCGTTGCAAACTGTCTCAACAGATGGCACTTGGGTTTCTGTCCCACTGATCAGACTTC 821
Qy 718 TTTTTCATCAATGTTGGTGACGCTCTACAGGTAAATGACTAATGGGAGGTTTAAAGTGTA 777
Db 822 TTTTTCATCAATGTTGGTGACGCTCTTTCAGGTAATGACTAATGGGAGGTTTAAAGTGTA 881
Qy 778 AAGCATAGGTTTGGCTGACACCAAGAGTCAAGGTTATCAATGATCTACTTTGGAGGA 837
Db 882 AAGCATAGGTTTGGCTGACACCAAGAGTCAAGGTTATCAATGATCTACTTTGGAGGA 941
Qy 838 CCAGCGTTCAGTGAAATAATAGCACTTTTCACTTCACTGATGTTTAAAGAGAGGAGTGT 897
Db 942 CCAGCGTTCAGTGAAATAATAGCACTTTTCACTTCACTGATGTTTAAAGAGAGAGTGT 1001
Qy 898 TTGTACAAAGAGTTCACATGTTGTAATACAGAGGCTGCGTACACTTTCAGGCTAGCT 957
Db 1002 TTGTACAAAGAGTTCACATGTTGTAATACAGAGGCTGCGTACCGTCAAGGCTAGCG 1061

QY 958 GATAATAGCTTGGCCCTTTCCAGAAATCTGCTGCTGAT 996
|||||
Db 1062 GATAATAGACTCGGCCCTTTTTCAGAAATCTGCTGCTGAT 1100
|||||

RESULT 3

US-09-719-108-7
; Sequence 7, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-719-108-7

Query Match 42.6%; Score 424.4; DB 3; Length 1237;
Best Local Similarity 67.5%; Pred. No. 3.5e-132;
Matches 612; Conservative 0; Mismatches 291; Indels 3; Gaps 1;
QY 79 ATTCTGTGGTGCAGCTCAAGCACCCTGATGCAAGATCTCATAGTGAAACCCCTGTAGG 138
|||||
Db 199 ATCCCGCTGCTCAACCTAGCCGATCCGGAAGCGAAACCCGAATCGTAAAGCCCTGCGAG 258
|||||
QY 139 GACTTCGGCTCTCAAGCTTGTGAACCATGGTGTTCATTTGAGTGAATGATGCCAATTTA 198
|||||
Db 259 GAGTTCGGGTTCTTCAAGGTCGTAAACCGGAGTCGACCCGAACTCATGACTCGGTTA 318
|||||
QY 199 GAAACGAGGCCCTCAGGTTCTTTAAATAATCTCAGTCGAGAAAGACAGAGCTGTCCTC 258
|||||
Db 319 GAGCAGAGGCTATTGGCTTCTTCGGCTTGCCTCAGTCTCTTAAACCGGCCGCTCCA 378
|||||
QY 259 CCCGACCCCTTTCGGTATGATGAGCAAGAGATGGCCCAACCGGTGATGCGTTGGGTG 318
|||||
Db 379 CCTGAACCGTACGGTTATGGTAAATAACCGATTTGGACCAACCGTGACGTTGGTGGATT 438
|||||
QY 319 GAATACCTCTCTCAACACCAACCTGATGATTTATCTACCCCAATCATTTCGATTTTC 378
|||||
Db 439 GAGTATCTCTCTCAATGCTAATCCTCAGCTCTCTCTCTCTTAAACCTCCGCCGTTTC 498
|||||
QY 379 CGAGAAATTCCTCATCATTTTCAGGGCGGTGGAGAACTACATACAGCAGTGAAGAAC 438
|||||
Db 499 CTTCAACCCCTCAATTTTCGTTGATGCGTGGAGGATCATGAGAGATTAAAGNA 558
|||||
QY 439 ATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGGTGGGATAGGCGAGAGGAATAGG 498
|||||
Db 559 GTGTCGTACAGGTGTTGAGATGTTGCCGAAGAACTAGGGATAGAGCAAGGGACACT 618
|||||
QY 499 TTAAGCAGGTTCTGAGAGATGAGAAAGTATTGCTGCTTCAGGTTGAACTACCCG 558
|||||
Db 619 CTGAGTAAATCTGAGAGATGAGAGAGTGAATCTGTCCTGAGACTAAACCATTTATCCG 678
|||||
QY 559 CTTGCGCCCTGAGTGCAGCACTGAACCGGAATTTGTTGGTGGTGGGAGCAGACAGAC 618
|||||
Db 679 GC---GGCGGAGGAGGCGGAGAGATGGTGAAGTGGGGTGGGGGAAACACAGAC 735
|||||
QY 619 CCACAGATAATTTCTGCTCTTAAGATCTTAACAGCACATCTGGCTTGCATAATCTGCTCTCA 678
|||||

Db 736 CCACAGATAATCTCAGTCTTAAGATCTAATAACACGGCGGGTCTTCAAAATCTGTGTGAA 795
QY 679 GATGCACTTGGGTTTTCAGTCCACCTGATCAGACTTCTCTTTTTCATCAATGTTGGTGAC 738
|||||
Db 796 GATGGAAGTTGGTGGCTGCTCCCTCTGATCACTCTTCTTCTTCAATTAATGTTGGAGAT 855
|||||
QY 739 GCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCATAGGGTTTGGCTGAC 798
|||||
Db 856 GCTCTTCAGGTTATGACTTAACGGGAGGTTCAAGAGTGTAAACACACAGGGTCTTAGCCGAT 915
|||||
QY 799 ACAAGAGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCGCTTTCAGTCAAAATATA 858
|||||
Db 916 ACAAGAGATCGAGATTTCATGATATATTTTCGGCGGACCGCCATTTAGCCAGAGATC 975
|||||
QY 859 GCACCTTTTACCTTCAGTGTATTAAGGAGGAGGAGTGTTTGTACAAAGAGTTCACATGG 918
|||||
Db 976 GCACCATTTGCCATGCTTGTCCCTGAGCAAGATGATTGGCTTTTACAAAGATTCACTTGG 1035
|||||
QY 919 TGTGAATCAAGAGGCTGCGTACACTTCAGGCTAGCTGATATAGGCTTGGCCCTTTC 978
|||||
Db 1036 TCTCAATACAAATCTTCTGCTTACAAAGTCAAGCTTGGTGTATATAGACTTGGTCTCTTT 1095
|||||
QY 979 CAGAAA 984
|||||
Db 1096 GAGAAA 1101
|||||

RESULT 4

US-09-614-912-13
; Sequence 13, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Cai, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-13

Query Match 42.3%; Score 421.4; DB 3; Length 1352;
Best Local Similarity 65.7%; Pred. No. 3.8e-131;
Matches 652; Conservative 0; Mismatches 326; Indels 15; Gaps 2;
QY 1 ATGGTGTGTTCTGCTCAGCCAGCATTTGAACCGATTTTCTCTTCTGAACCATTTCAAGTCC 60
|||||
Db 159 ATGGTGTGTTGTTCCAAAGCAACACAGAAATAATCTCTCTACATTAAGAACTGTCATCCA 218
|||||

; PRIOR FILING DATE: 1998-06-12									
; PRIOR APPLICATION NUMBER: GB 9815404.0									
; PRIOR FILING DATE: 1998-07-15									
; NUMBER OF SEQ ID NOS: 16									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 9									
; LENGTH: 1008									
; TYPE: DNA									
; ORGANISM: Arabidopsis thaliana									
US-09-719-108-9									
Query Match 38.3%; Score 381.6; DB 3; Length 1008;									
Best Local Similarity 64.7%; Pred. No. 8.5e-118; Indels 6; Gaps 1;									
Matches 586; Conservative 0; Mismatches 314;									
QY	79	ATTCTGTGGTTCGACCTCAGCAGCCCGATGCCAAGATCTCATAGTGAACCGCTGTAGG	138						
DB	79	ATCCCTGTTATAGACTTAACCGACTCAGATGCCAAACCCAAATCGTCAAGCATGTAA	138						
QY	139	GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTGGAGTTAATGGCCAAATTA	198						
DB	139	GAGTTTGGGTCTTCAAGATCATCAACCATGGGTCCGACCCGATCTTTTGACTCAGTTG	198						
QY	199	GAAACGAGCCCTCAGGTTCTTTTAAAAATCTCAGTCCGAGAAAGACAGAGCTGTCCC	258						
DB	199	GAGCAAGAAGCCATCAACTTCTTTGCTTTGTCATCACTCTCTCAAGAGCAAAAGCGGTCCA	258						
QY	259	CCGACCCCTTCGGCTATGGTAGCAAGAGGATTTGCCCAACCGGTGATGTCGGTTGGGTC	318						
DB	259	CCTGACCCCTTGGTTACGGTACTAAAGGATTTGACCCAAATGGTGACCTTGGCTGGCTT	318						
QY	319	GAATACCTCTCTCTCAACACCAACCCCTGATGTATCTCACCCAAATCACTTTGCAATTTTC	378						
DB	319	GAGTACATTTCTCTTAATGCTAATCTTTGCTTGGTGTGATCTCAAAAACACCGCATTTTC	378						
QY	379	CGAGAAAATCCTCATCATTTCAAGGCGGTGGTGGAGAACTACATTACAGCAGTGAAGAAC	438						
DB	379	CGGCACACCCCTGCAATTTTCAGAGAGGCAGTGGGAAGAGTACATTAAAGAGATGAAGAGA	438						
QY	439	ATGTGCTATCGGTGTGCAATTTGATGGCGAGGGTTGGGATTAAGGCAGAGCAATACG	498						
DB	439	ATGTGAGCAAAATTTCTGGAATGGTAGAGGAAGAGCTAAAGATAGAGCCAAAGGAGAAG	498						
QY	499	TTAAGCAGGTGTGCTGAAGATGAGAAAAAGTGAATTCGTCTTTCAGGTGTGAACCACTACCCG	558						
DB	499	CTGAGCCGTTTGGTGAAGTGAAGAAAGTGAATTCGTGCTGAGAAATGAACCACTATACCG	558						
QY	559	CCTTGCCCTGAGGTGAAGCACTGAACCGGAATTTGGTGGGTTTGGGGAGCACACAGAC	618						
DB	559	-----GAGAAGGAGAGACTCCGGTCAAGGAAGAGATTGGGTTCGGTGAGCACACTGAT	612						
QY	619	CCACAGATAATTCTGCTTAAGATCTAACAGCACTCTGGCTTGCAAACTGCTCTACA	678						
DB	613	CCACAGTTGATATCACTGCTCAGATCAAAACGACACAGAGGGTTTGCANATCTGTGCAAA	672						
QY	679	GATGGCACTTGGGTTTCAGTCCACCTGATCAGACTTCTTTTTCATCAATGTTGGTGAC	738						
DB	673	GATGGAACATGGGTGATGTTACACTGATCACTCTCTTCTTCTTCTTGTTCGGAGAT	732						
QY	739	GCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCATAGGGTTTTCGGCTGAC	798						
DB	733	ACTCTTCAGGTGATGACAAACGGAAGATTCAAGAGTGTGAAACATAGAGTGGTGACAAAT	792						
QY	799	ACNACCAAGTCAAGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAATAATA	858						
DB	793	ACAAAGAGTCAAGGATATCGATGATCTACTTCGACAGTCTCTCTTTTGAGCGAAGATT	852						
QY	859	GCACCTTTACCTTCAGTGTATGTTAAAGAGAGGAGTGTGTTGTACAAAGAGTTTCACATGG	918						
DB	853	GCACCAATATATGCTTGTGCAAGCAAGATGATTCGCTTTTATATGATTTACTTGG	912						
QY	919	TGTGAATACAAGAAGGCTCGCTACACTTCAAGGCTAGCTGATTAATAGGCTTTGCCCTTTC	978						

Db	913	TCTCAATCAAGTTATCTGCTTACAAAACTAAGCTTGTGTACTATAGGCTTGGTCTCTCTTT	973						
QY	979	CAGAAA 984							
DB	973	GAGAAA 978							

RESULT 8									
US-09-614-912-7									
; Sequence 7, Application US/09614912									
; Patent No. 6677502									
; GENERAL INFORMATION:									
; APPLICANT: Allen, Steve									
; APPLICANT: Rafalski, Antoni									
; APPLICANT: Orozco, Buddy									
; APPLICANT: Miao, Gou-Hau									
; APPLICANT: Famodu, Omolayo O.									
; APPLICANT: Lee, Jian Ming									
; APPLICANT: Sakai, Hajime									
; APPLICANT: Weng, Zude									
; APPLICANT: Caimi, Perry G									
; APPLICANT: Anderson, Shawn									
; TITLE OF INVENTION: Plant Metabolism Genes									
; FILE REFERENCE: BBI378 US NA									
; CURRENT APPLICATION NUMBER: US/09/614,912									
; CURRENT FILING DATE: 2000-07-12									
; PRIOR APPLICATION NUMBER: 60/143,401									
; PRIOR FILING DATE: 1999-07-12									
; PRIOR APPLICATION NUMBER: 60/143,412									
; PRIOR FILING DATE: 1999-07-12									
; PRIOR APPLICATION NUMBER: 60/146,650									
; PRIOR FILING DATE: 1999-07-30									
; PRIOR APPLICATION NUMBER: 60/170,906									
; PRIOR FILING DATE: 1999-12-15									
; PRIOR APPLICATION NUMBER: 60/172,959									
; PRIOR FILING DATE: 1999-12-21									
; PRIOR APPLICATION NUMBER: 60/172,946									
; PRIOR FILING DATE: 1999-12-21									
; NUMBER OF SEQ ID NOS: 204									
; SOFTWARE: Microsoft Office 97									
; SEQ ID NO 7									
; LENGTH: 1473									
; TYPE: DNA									
; ORGANISM: Triticum aestivum									
US-09-614-912-7									
Query Match 36.4%; Score 362.6; DB 3; Length 1473;									
Best Local Similarity 61.5%; Pred. No. 2.8e-111;									
Matches 603; Conservative 0; Mismatches 369; Indels 9; Gaps 1;									
QY	2	TGGTGTGTTCTGTCTCAGCCAGCATTTGAACAGTCTTTTCTCTCTGMAAACCAATTCAGTCCA	61						
DB	128	TGGTCTCGCCAGCAGCCCGCGTGGTGCATCATCCCGTCTCTCAGGTGCGCGACCCCG	187						
QY	62	CGCCCTTGTTCACGGGAGTTCTGTGTGTCGACCTCACGCCACCCCGATGCCAAGAATCTCA	121						
DB	188	GGGACTACTTCTCCGGCATGCCGTGGTGCAGCTCTCCAGCCCTGCGCGCGCGCGGCCA	247						
QY	122	TAGTGAACCCCTGTAGGAGACTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCATTGG	181						
DB	248	TCGCCAGCCTGCGAGCGCTTCGGGTTCCTTCAAGCTGTCAACCAACGCGGGTGC	307						
QY	182	AGTTAATGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGA	241						
DB	308	ACAGATGACAGGCTCGAGTCGAGTGCGAGGCCCGTTCAGGTTCTTCTCGTGCAGCGCGGACA	367						
QY	242	AAGACAGAGCTGGTCCCGCCGACCCCTTTCGGCTATAGGTAGCAAGAGATTGGCCCAACG	301						
DB	368	AGGACCGCTCCGGCCCGGCTACCCGTTCCGGTTCGCGTACGCGACGAAGCATCGGGCTCAATG	427						
QY	302	GTGATGTGGTGGGTTCGATACCTCTCTCTCAACACCAACCCCTGATGTATTCTCACCCA	361						
DB	428	GCACATGGGGTGGTTCGAGTACCTCTCTCGCGCTCGACTCCCGCTCGCTCTCCGGCG	487						

QY 362 AATCACTTTGCAATTTCCAGAAATCCTCATCATTTTCAGGGGGTGGTGGAGAACTACA 421
 Db 488 CTTGGCCCGTCCGCTCTCG-----CGCTCTCCGGCGCGCTGAAACGAGTACA 538
 QY 422 TTACAGCAGTGAAGAACATGTCTATGCGGTGTTGGAATTTGATGGCGGAGGGTGGGGA 481
 Db 539 TCGGGCGGTGCGAAGGTGGCGGTGCGGTGATGAGCGCATGGCGGAGGGCTGGGCA 598
 QY 482 TAAGCAGAGGAATACGTTAAGCAGGTGTCTGAAGGATGAGAAAGTGAATTCGTGCTTCA 541
 Db 599 TTGGCGCGCTGACGCGCTGAGCGGATGTGTGACGCGGAGGGGACGACAGGTGTTCC 658
 QY 542 GGTGGAACACTACCGCGCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTGGGT 601
 Db 659 GGTGGAACACTACCGCGCTGCGACGCGCTGCGGGGTGGGCTGCGAGCCACCGGCT 718
 QY 602 TTGGGAGGACACAGACCCACAGATAATTTCTGTTAAGATCTAACAGCACATCTGGCT 661
 Db 719 TCGGCGAGCACAGGACCGCGAGCTCATCTCGTGTGCGCTTCAACGCGCAGTCCGGCC 778
 QY 662 TCGAAATCTGTCTCAGATGGCCTTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTTT 721
 Db 779 TCGAGATCGGCTCCAGAACGGGAGTGGGTGTCGTCGCTCGGACCGGACGCTTCT 838
 QY 722 TCATCAATGTTGGTGAACGCTCTACAGGTAAATGACTAATGGGAGGTTTAAAGTGTAAGC 781
 Db 839 TCGTCAACGTCGCGACTCTGTCAGGTGCTGACCAACCGGAGGTTCAAGAGCGTGAAGC 898
 QY 782 ATAGGGTTTGGCTGACACACGAGTCAAGGTATCATGATCTACTTTGAGGACCGAG 841
 Db 899 ACAGGGTGGTGGCCCAACAGCCTTAAAGTCTAGGGTTTCCATGATCTACTTTGAGGGCCAG 958
 QY 842 CGTTGAGTGAATAATAGCACCTTTACCTTTCAGTGTATGTTTAAAGGAGAGGAGTGTGTT 901
 Db 959 CAATGACACAGAGGATGACCAATGTCGCCAGCTGCTGGGCGGAGGAGCAGGCTGT 1018
 QY 902 ACAAGAGTTCATGTTGTGAATACAAAGAGGCTGCGTACACTTCAAGGGCTAGCTGATA 961
 Db 1019 ACAAGAGTTCATGTTGGGCGAGTACAAAGGCTGCTTCAACTCCAGGCTCGGGGACA 1078
 QY 962 ATAGGCTTGGCCCTTTCGAGA 982
 Db 1079 ACAGGCTGGCTCAGTTCACCA 1099

RESULT 9

US-09-719-108-5
 ; Sequence S, Application US/09719108
 ; Patent No. 6670527
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Stephen G
 ; APPLICANT: Hedden, Peter
 ; APPLICANT: Phillips, Andrew L
 ; TITLE OF INVENTION: Gibberellin 2-Oxidase
 ; FILE REFERENCE: 0623.0970000
 ; CURRENT APPLICATION NUMBER: US/09/719,108
 ; CURRENT FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: PCT/GB99/01857
 ; PRIOR FILING DATE: 1999-06-11
 ; PRIOR APPLICATION NUMBER: GB 9812821.8
 ; PRIOR FILING DATE: 1998-06-12
 ; PRIOR APPLICATION NUMBER: GB 9815404.0
 ; PRIOR FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1318
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1243, 1265)

OTHER INFORMATION: unidentified residue
 US-09-719-108-5

Query Match 35.8%; Score 356.6; DB 3; Length 1318;
 Best Local Similarity 63.2%; Pred. No. 2.8e-109;
 Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;
 QY 65 CTTTGTTCAGGGGATTCCTGTGTGCGACCTCACGACCCCGATGCCAAGAATCTCATAG 124
 Db 78 CCGGGTCTCTCTAATCCGGTTATAGATATGTCTGACCCAGAAATCCAAATGCCCCG 137
 QY 125 TGAACGCTGTAGGACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATTGGAGT 184
 Db 138 TGAAGACATGCGAAGACTTCGGCTTCTCAAGGTGATCAACCATGGCTTTCGAGAGC 197
 QY 185 TAATGCCCAATTTAGAAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGAAAG 244
 Db 198 TAGTCTCTGTTTAAACACAGAGACCGTCGATTTCTTCTCGTGGCCCAAGTCAGAGAAA 257
 QY 245 ACAGAGTGGTCCCCCGACCCCTTTCCGCTATGTGTAGCAAGAGGATTTGGCCCAACGGTG 304
 Db 258 CCCAAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAAGATTTGGTCGGAATGGTG 314
 QY 305 ATGTGCGTTGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCCCAAT 364
 Db 315 ACGTGGGTGGGTGAGTACTTGTGTGATGAACGCTTAATCATGATTCGCGTTCGGGTCCAC 374
 QY 365 CACTTTGCAATTTCCGAGAAAAATCCTCATCTTCAGGGCGGTGGTGAGAACTACATTA 424
 Db 375 TATTTCCAAAGTCTTCTCAAAAGCCCGGAACTTTTCAGAAAACGATTTGGAAGAGTACACAA 434
 QY 425 CAGCAGTGAAGAACATGTCTATGCGGTGTTGGAAATGTATGGCGGAGGGTGGGGATAA 484
 Db 435 CATCAGTGAGAAAAATGACATTCGATGTTTGGGAAGATCACAGATGGGTAGGGATCA 494
 QY 485 GCAGAGAAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTCAGGT 544
 Db 495 AACCGAGGAACACACTTAGCAAGCTTGTCTCGACCAAAACACGAGCTCGATATTGAGAG 554
 QY 545 TGAACCACTACCGCGCTTGGCCCTGAGGTGCAAGCACTGAAC-----CGGAATTCG 595
 Db 555 TTAATCACTATCCACCATGTCTCTTAGCAATAAGAAAACCAATGGTGTGAAGAATGTGA 614
 QY 596 TTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGTTTAAAGATCTAACAGACAT 655
 Db 615 TTGGTTTGTGTGAACACACAGATCTCAATCATCTCTGTCTTAAAGATCTAACACACTT 674
 QY 656 CTGGCTTGCATAATCTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTT 715
 Db 675 CTGGTCTCCAAATTAATCTAAATGATGGCTCATGGATCTCTGTCTCCCTCCCGATCACACTT 734
 QY 716 CTTTTCATCAATGTTGGTGAACGCTCTACAGGTAATGACTAATGGAGGTTTAAAGTG 775
 Db 735 CTTCTTCTTCAACGTTGGTGACTCTCTCCAGGTGATGACAAATGGGAGTTTCAAGAGCG 794
 QY 776 TAAAGCATAGGGTTTGGCTGACACAAACGAAAGTCAAGGTTATCAATGATCTACTTTGAG 835
 Db 795 TGAGGCATAGGGTTTGTAGCTAACTGTAAATAATCTAGGGTTTCTATGATTTACTTCGCTG 854
 QY 836 GACCAAGCTTGAAGTGAATAATAGCACTTTACCTTTCAGTGTGATGTTAAAGGAGGAGT 895
 Db 855 GACCTTCATTGACTCAGAGAAATCGCTCCGTTGACATGTTTGATAGACAATGAGGACGAGA 914
 QY 896 GTTTGTACAAAGAGTTACATGGTGTGAATACAAAGGCTGCGTACACTTCAAGGCTAG 955
 Db 915 GGTGTACGAGGAGTTTACTTTGGTCTGAATCAAAAACTCTACCTTACAACTCTAGATTGT 974
 QY 956 CTGATAATAGGCTTGGCCCTTTCCAGA 982
 Db 975 CTGATAATAGGCTTCAACAATTCGAAA 1001

RESULT 10


```
US-09-614-912-3
; Sequence 3, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-614-912-3

Query Match 35.5%; Score 354; DB 3; Length 1650;
Best Local Similarity 60.9%; Pred.No.2.4e-108;
Matches 598; Conservative 0; Mismatches 375; Indels 9; Gaps 1;

QY 2 TGGTGTCTCTGCTCAGCCAGCATTTGAACACCGTTTTCCTCTGAAACCATCAAGTCCA 61
Db 132 TGGTGTCTCTGCTGCGCGCGCGCGTGCATCACATCCCGTGTCTGAGGTGCGCGACCCCG 191
QY 62 CGCCCTTGTTCACGGGATTCCTGTGGTGCACCTCAGCACCCCGATGCCAAGAATCTCA 121
Db 192 GCACGCTCTTCTCCGGCGTCCGGTCTGTCGACCTCGGCAGCCCGCGCGGAGGCGCG 251
QY 122 TAGTGAACCGCTTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTCCATTG 181
Db 252 TGGTGACGCTTCGAGCGGTACGGGTCTTCAAGGTCTGTCACCAACGCGGTGGCCACGG 311
QY 182 AGTTAATGGCCAAATTTAGAAAAACGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGA 241
Db 312 ACAGATGACACAGCGCGAGTCGAGGCGCTCAGGTCTTCTCCAGACGCGACCGACA 371
QY 242 AGACAGAGCTGTGTCGCCCGACCTTTCGGGTATGGTAGAAGAGATTGGCCCAACG 301
Db 372 AGACCGCTCCGCGCGCGCTACCCGTTCCGGTACGCGACGAAGCGATCGGGTTCATG 431
QY 302 GTGATCTCGGTGGGTTCGATACCTCTCTCAACCAACCAACCTGATGTTATCTCACCCA 361
Db 432 GCACATGGGGTGGCTCGAGTACTCTCTCTCGCCCTCGACGACGGTCTCGCCGACG 491
QY 362 AATCACTTTGCAATTTCCGAGAAAAATCTCATATTTCAAGGGCGGTGGTGAGAACTACA 421
Db 492 CCTGCACCGTCCGCTCTCTGCG-----CGGTCTTCGCGGCGCTCTGAACGAGTACA 542
QY 422 TTAACAGAGTGAAGACATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGGTGGGA 481
Db 543 TCTCGGGGTGCGGAAGGTGGCGGTGCGGGTGTGAGGGCGATGTCGGAGGGGCTGGGCA 602
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QY 482 TAAGCAGAGGAATACGTTAAAGCAGGTTGCTGAAGATGAGAAAAAGTATTCGTGCTTCA 541
Db 603 TTGCGCAGCGCGACGCGCTGAGCGCGCTGGTGACGCGGAAGGAGCGACCAAGGTGTTCC 662
QY 542 GGTTCGAACCACTACCGCGCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGT 601
Db 663 GCGTGAACCACTACCGCGCGCTGCGCGCGCTGCGCGCGCTCGGCTGCGAGCGTCAACGGCT 722
QY 602 TTGGGGAGCACACAGACCCACAGATAAATTTCTGTCTTAAGATCTAACAGCAATCTGGCT 661
Db 723 TCGGGAGCACACCGACCCGCGAGCTCGTCTCGTCTCGCTCAAAACGCAAGTCCGGCC 782
QY 662 TGCAAAATCTGTCTCACAGATGGCACTTGGGTTTTCAGTCCACCTGATCAGACTTCTTTT 721
Db 783 TGCAGATCGCGCTCCGCGACGCGCGAGTGGGTGTCGTCGCTCCGCTCCGACCGCGACTCTTCT 842
QY 722 TCATCAATGTGGTGACCGCTCTACAGGTAACTAATGGGAGGTTTAAAGTGTAAAGC 781
Db 843 TCGTCAACGTCGCGCACTCGTTGCAGGTTCTGACCAATGGGAGGTTCAAGAGCGTGAAGC 902
QY 782 ATAGGGTTTTGGCTGACACAAACGAAAGTCAAGGTTTCAATGATCTACTTTGGAGGACAG 841
Db 903 ACAGGGTGGTGCCCAACAGCCTTAAAGTCTAGGGTTTCTTCACTACTTTGGAGGGCCAC 962
QY 842 CGTTGAGTGAAATATATAGCACCTTTTACCTTTCAGTGTGATGTATAAAGGAGAGGAGTGT 901
Db 963 CGTTAGCACAGAGGATTCACCATTTGCCACAGCTGCTGGGGGAGGAGAGCAGAGCCTGT 1022
QY 902 ACAAGAGTTTCATGGTGTGTAATACAGAAGAGGCTGCGTACACTTCAAGGCTAGCTGATA 961
Db 1023 ACAAGAGTTTCATGGGATGAGTACAAGAGGCTGCGCTTACAAATCAAGGCTTGGAGACA 1082
QY 962 ATAGGCTTGCCCTTTCCAGAA 983
Db 1083 ACAGGCTGCCAGTTTGAA 1104

RESULT 11
US-09-614-912-1
; Sequence 1, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1555
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; TYPE: DNA
 ; ORGANISM: Zea mays
 US-09-614-912-1

Query Match	31.5%	Score 314.2	DB 3	Length 1555
Best Local Similarity	59.3%	Pred. No. 6.3e-95		
Matches	576	Conservative 0	Mismatches 383	Indels 12
	Gaps	2		
Qy	16	CAGCGACGATTTGAACCAAGTCTTTCTTCTGAAACCAATTC	AAAGTCCACGCGCCCTTGTTCACG	75
Db	136	CGCGCTGTCGACGAGATCCCGCTCTCTGGGTCCCGGGCC	CCGAGGACAGCTTCTCG	195
Qy	76	GGGATTCCTGTGTGTCGACCTCACGCA	CCCGGATGCCAAGAAATCTCATGTGAAGCCCTGT	135
Db	196	GGAGTGC	CGGTGCTGCACTGTCAGGACACGCGCGCGCGGGCGATCGTGCAGCGCCTGC	255
Qy	136	AGGACATTCGGCTTCTTCACAGTCTGTGAA	CCATCGTTCATTTGGAGTTAAATGGCCAAAT	195
Db	256	GAGCGCTTCGGGTCTTC	CAAGTCTGTAACACCGCGTGGCCGCGGCCACCCATGGAAGG	315
Qy	196	TTAGAAAAAGAGGCGCCTCAGGTTCTTTTAAAAAATCT	CAGTCCGAGAAAGACAGAGCTGGT	255
Db	316	GCCGAGTCCGAGGCGGT	CAGGTTCTTCGCGCAGGCGCAGGCGGACAAAGGACCGCGCGGG	375
Qy	256	CCCCCGACCCCTTTCGGCTATGCTAGCA	GAGGAAATGGCCCAAACGGTGATGTCGGTTGG	315
Db	376	CCGCGGTACCGGTTTCGGGTACGGCAGCA	AGCGGATCGGGGTCTCATGTCGCAATCGGGGTGG	435
Qy	316	GTGCAATACCTCCCTCTCAACACCA	CCCTCATGTTATCTCACCCAAATCACTTTGCAAT	375
Db	436	CTCGAGTACCTCTCTCTCGCGT	CGAGCGCTCTCCGACGCTGCCCGCTGCC	495
Qy	376	TTCCGAGAAATCTCATCATTTTCAGGCG	GGTGTGGAGAACTACATTCACAGCAGTGAAG	435
Db	496	TCCAGCG-----	CCGCGTTCCGAGCGCGCTGAACGAGTACGTCGCGCGCTGCGG	546
Qy	436	AACATGTCTATGCGGTGTTGGAATTCATG	CGCAGGSGTTGGGATAAGCAGCAGGAAT	495
Db	547	AAGTGGCGGGCGGTGCTGAGGCG	ATGTCGAGGCGCTGGGCATTTGGACCGCGAC	606
Qy	496	ACGTTAAGCAGGTTGCTGAAGGATGAGAAA	AGTGAATTCGTGCTTCAGGTTGAACCACTAC	555
Db	607	CGCTGAGCTCCATGGTGAGCGCG	CGGGAGCGACCAAGGTGTTCCGCGTGAACCACTAC	666
Qy	556	CGCGCTTCGCTGAGGTGCAAGCACTGAA	CCGGAAATTTGGTTGGGTTGGGAGCACACA	615
Db	667	CGCGCTTCGCGCGCTGCAGGGCT	TCGGCTGCAGCACCGGGCTTCGCGCAGCACACC	726
Qy	616	GACCCACAGATAATTTCTGCTTAAGATCT	AAACAGCACATCTGGCTTGCAAAATCTGTCTC	675
Db	727	GACCCGAGATCATCTCGTGCT	CCGCTCCAAACGGCACCTCCGGCTTCAGATCGCGCTC	786
Qy	676	ACAGATGGCAC- - -	TTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCAATGTT	732
Db	787	CGCGACCGCGCAGTGGGTCTCGGTG	CCCTCCGACCGCAGCGCTCTTCGTTAAGCTC	846
Qy	733	GGTGACCTCTACAGGTAATGCACTAAT	TGGGAGGTTTAAAGCTAAGCATAGGTTTTC	792
Db	847	GGCGACTCGTTCGAGGTGCTGACCAAC	CGGAGGTTTCAGGACGCTGAAGCACCGGGGTGGT	906
Qy	793	GCTGACACAAAGAGTCAAGGTTATCAAT	GATCTACTTTTGAGGACACAGCGTTGAGTGAA	852
Db	907	ACCAACAGCTCAAGTCCAGAGTTTCCTT	CATCTACTTCGCGGGCGCGCGCTGGGGCAG	966
Qy	853	AATATAGCACTTTTACCTTCAGTGAATGTT	TAAAGGAGGAGGTGTTTGTATACAAAGATTTC	912
Db	967	CGGATCGCGCGCTGCGCGAGGTGCTG	ACGAGGAGGAGGAGGAGCCCTGTATCAAGGAGTTC	1026
Qy	913	ACATGGTGTGAATACAAAGAGGCTGCG	TACACTTTCAGGCTTAGCTGATAATPAGCTTGCC	972
Db	1027	ACGTGGGGCGAGTACAAAGAGCGCG	CGTACAAGACGAGGCTTCGGGCAACACAGGCTGCGC	1086
Qy	973	CTTTTCCAGAA	983	

Db 1087 CAGTTTGAGAA 1097

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RESULT 12
US-09-371-307-67
; Sequence 67, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 67
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (726)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-67

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Query Match	30.9%	Score 307.8;	DB 3;	Length 783;
Best Local Similarity	70.2%;	Pred. No. 5.8e-93;		
Matches 436;	Conservative 0;	Mismatches 167;	Indels 18;	Gaps 1;
Qy	391	CATCATTTTCAGGCGGTGGTGGAGAACTACATTTACAGCAGTGAAGAACATGTGCTATGCG	450	
Db	52	CAAACTTTGAGGTGGCTTTTGAATATATATGAAATCAGTAAAGAAATTGGCGTGTGAG	111	
Qy	451	GTGTTGGAAATTGATGGCGGAGGGGTTGGGATTAAGGCAGAGGAATACGTTTAAGCAGGTTG	510	
Db	112	ATACTTGAAATGATGCTGATGGTTGAAGATACAAACCCAGGAATGTGTTGAGCAAGCTG	171	
Qy	511	CTGAAGATGAGAAAAGTGAATTCGTGTCCTCAGGTTGAAACCACTACCCGCCCTTGCCTTGAG	570	
Db	172	TTGATGATCAAGAGAGTGACTCTGTGTTTCAGGGTGAATCATTTACCCACCATGCCCTTAAT	231	
Qy	571	GTCCAGCAGCTG-----AACCGGAAATTTGGTTGGGTTGGGGAGCAC	612	
Db	232	GTTCAACCTTTGAGTGGTAAATGGCAATGGGGATGTGATTTGGTTGGTGAACAC	291	
Qy	613	ACAGACCCACAGATAATTTCTGTCTTTAAGATCTAACACGACATCTGGCTTGCAAATCTGT	672	
Db	292	ACTGATCCACAATATCTCAGTGTTCAGATCTAACACACATCTTGGCTTCCAAATCTCT	351	
Qy	673	CTCACAGATGGCACTTGGGGTTTCAGTCCCACTGTATCAGACTTCTCTTTTTTCATCAATGTT	732	
Db	352	CTAAGAGAGGAAGCTGGATTTTCAGTGGCCACCTTGACCAACCTCATTTCTTCATCAATGTT	411	
Qy	733	GGTGAGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGAGTGTAAAGCATAGGGTTTGG	792	
Db	412	GGTGACTCTCTTACAGGTAATGACCAATGGAAGGTTTAAAGTGTAAACATAGGGTAGTG	471	
Qy	793	GCTGACACACGAGTCAAGGTTTATCAATGATCTACTTTGGGAGACACAGGTTTGAGTGAA	852	
Db	472	ACCAACAGTGTGAAATCAAGGCTATCAATGATTTATTTTGGTGACACCATTTGAGTGAG	531	
Qy	853	AATATAGCACTTTTACCTTCAGTGATGTTTAAAGGAGGAGGAGTGTGTTGTAACAAGAGTTC	912	
Db	532	AAATATAGCACTTTTGCCATCTTTTGATGAGAGGTGATCAACAAGAGCTTATATAAGAAATTT	591	

[illegible]

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RESULT 13
US-09-371-307-71
; Sequence 71, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: M08T:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 811
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-307-71

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Query Match	16.7%	Score 166;	DB 3;	Length 811;
Best Local Similarity	55.8%;	Pred. No. 4.3e-45;		
Matches 316;	Conservative 0;	Mismatches 250;	Indels 0;	Gaps 0;
QY	418	TACATTACAGCAGTGAAGACATCTGCTATGCGGTGTGGAAATGATGCGGAGGGGTG	477	
DB	2	TACACGTTGGCGTTCGGCGGATGGCGTCCCGGTCTGGAGCTGATGCGGAGGGGTG	61	
QY	478	GGGATAAGGCAGAGGAATACCTTAAGCAGGTTGCTGAAGGATGAGAAAAAGTGAATTCGTGC	537	
DB	62	GGCATCCCGCGCGCGCGGACGCGGTGCTGGCGCGGTGTGGCGCGCGGACGACG	121	
QY	538	TTACAGTTGAACCACTACCCGCCCTTGCCCTGAGGTGCAAGCACTGAACCGGAAATTTGGTT	597	
DB	122	GACTGCATGCTGCGGGTGAACCACTACCCGCGCGCGCGGTCAACCCAGGCTCAAG	181	
QY	598	GGGTTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCT	657	
DB	182	GGGTTCCGCGAGACACACCGACCCGACATCATCTCGGTGCTCCCGCGCAACGGACCTCC	241	
QY	658	GGCTTGCAAACTGCTCTCACAGATGGCACTTGGGTTCAGTGCCACCTGATCAGACTTCC	717	
DB	242	GGCTGAGATCGCGCTTCGGGACGGCGCTCGGCGCTCCGTCGCCCGCAGCGGGACGCC	301	
QY	718	TTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTTAAAGTGTA	777	
DB	302	TTCTTCGTCAACGTCGGCGACACCTGCAGGTGTTGACGAACGGGAGGTTTCAGGAGCGTG	361	
QY	778	AAGCATAGGGTTTTGGCTGACACAAACGAGTCAAGGTTATCAATGATCTACTTTGGAGGA	837	
DB	362	AGGCAACAGGGTGTGGTGAAACAGCGAGAGGTCCCGGGGTGTCATGTGTTCTTTCGGCGGC	421	
QY	838	CCAGGTTGAGTGAATAATATAGCACTTTTACCTTCAGGTGATGTTTAAAGGAGAGAGGTGT	897	
DB	422	CCGCGCGCGCGAGAGGCTGGGCGCGCTTCGGAGCTCTTCGGCGAGCGGCGCGCGAGC	481	
QY	898	TTGTACAAAGAGTTTCACATGTTGTGAATACAAAGAGGCTGGGTATACATTTCAAGGCTAGCT	957	

RESULT 15

US-09-371-307-68

Db 482 CGGTACCGGACTTCACTGGACGAGTTCAAGACCAAGCGGGTGCAGGACCAAGCTCGCG 541

Qy 958 GATAATAGGCTTGCCCTTTCAGAA 983

Db 542 GAAGACCGCGCTGTCGGCTTCAGAA 567

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RESULT 14
US-09-371-307-66
; Sequence 66, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R..
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 66
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (178)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-66

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Query Match	15.6%	Score 155.6;	DB 3;	Length 403;
Best Local Similarity	63.2%;	Pred. No. 8.9e-42;		
Matches 261; Conservative	0;	Mismatches 140;	Indels 12;	Gaps 1;
QY	217	TTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCGACACCTTTCCGGCTAT	276	
DB	2	TTCTTTCTCTATGTCACTCAATGAAGAAAAAGTAGGACCTCCCAATCCATTGGGTAT	61	
QY	277	GGTAGCAAGAGGAATTTGGCCCAACCGGTGATGTTCGGTTGGGTGGAATACCTCTCTCTCAAC	336	
DB	62	GGTAGCAAGAAAAATTGGACAAATGGGGACGTTGGTTGGAATTGAGTACCTTCTTCTCAAC	121	
QY	337	ACCAACCCGTGATGTTATCTCACTACCCCAAATCACTTTTGCACTTTTCCGAGAAAAATCCTCATCAT	396	
DB	122	ACCAATCAAGAACACAACT-----TCTCTGTTTATGGCAAAAACCTTGAGAAA	169	
QY	397	TTCAGGCGCGTGTGGAGAACTACATTACACGAGTGAAGAACATGTGCTATCGGGTTTG	456	
DB	170	TTCAGGTGNCCTGTTGAACAGTTACATGCTCTTCGTGAGGAAGATGGCATGTGAGATTCCT	229	
QY	457	GAATTGATGGCGAGGGGTTGGGGATTAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAG	516	
DB	230	GAGTTGATGCGCAGAGGGTTGAAGNTTCAGCAAAAGGATGTTTGTAGCAAGCTTCTTAATG	289	
QY	517	GATGAGAAAAAGTCATTCTGTCCTTCAGGTTCAACCCACTTACC CGCCTTGCCCTGAGGTGCAA	576	
DB	290	GATTAACAAGTAGACTCTATTCTTTCAGGGTGAATCATTTACGCTGCTGCTGAAATGACT	349	
QY	577	GCAC TGAACCGGAATTTGGTTGGGTTGGGGAGCAACACAGACCCACAGATAAT	629	
DB	350	CTGAATGATCAGAACTTGATTGGGTTTGGAGAACACACAGACCCACAAATCAT	402	

RESULT 15

US-09-371-307-68


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; Sequence 68, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (306)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-68

Query Match      15.5%; Score 154.8; DB 3; Length 406;
Best Local Similarity 66.6%; Pred. No. 1.7e-41;
Matches 279; Conservative 0; Mismatches 113; Indels 27; Gaps 3;

QY 247 AGAGCTGGTCCCGACCCCTTTCGGCTATGCTAGCAGAGGATGGCCCAACCGGTGAT 306
Db 2 AAAACAGNACACCCCGCCTTATGGCTATGTAATAAAGGATGGACCAATGGTGAT 61

QY 307 GTCGGTTGGTGGATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCCAAATCA 366
Db GTTGGTTGGTGGATATCTCTCTCAACCAACCAAG-----ACCCGAATCT 111

QY 367 CTTTGCATTTCCGAGAAATCTCATCTTTCAGGCGGTGGTGAGNACTACATTACA 426
Db 112 CCTTGGAACT-----GAAACCCAGAGAGTTTCAGGATTTGGATAATTATATGGCA 166

QY 427 GCAGTGAAGACATGTGCTATGCGGTGTTGGAATTGATGGCGAGGGTTGGGGATAAGG 486
Db 167 GCAGTGAAGAAATGGCATGTGAGATCTTGAATGATAGCTGTGGCTAAGGTTGAG 226

QY 487 CAGAGGAATA CGTTAAGCAGGTTGCTGAAGGATGAGAAAGTATTCGTGCTCAGGTTG 546
Db 227 CCAAGAAATGTTTAAAGTAAGCTGATGATGGATGAACAGAGTACTCTGTTTTCAAGGCTG 286

QY 547 AACCACTACCCGCTTGCCCTGAG-----TGCAAGCACTGAACCGGAATTTG 594
Db 287 AACCACTACCCCTCCGTCGAGAGGTTTCAGTCCCTGGAATGGAACGAGCAGTAATGTG 346

QY 595 GTTGGTTTGGGGAGACACACACAGATAATTTCTGCTTAAGATCTTAACAGCAC 653
Db 347 ATTGGATTCCGGTGAACACACTGACCCACAAATCAITTCAGTCCTAAGATCCAAACAC 405
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-670-454-1_COPY_68_1063

Perfect score: 996

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Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main:*

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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	996	100.0	999	8	US-10-821-711-3	Sequence 3, Appli
2	996	100.0	1318	8	US-10-670-454-1	Sequence 1, Appli
3	827.4	83.1	1359	3	US-09-371-307-62	Sequence 62, Appli
4	827.4	83.1	1359	6	US-10-401-321-62	Sequence 62, Appli
5	424.4	42.6	1026	3	US-09-938-842A-1350	Sequence 1350, Ap
6	424.4	42.6	1026	3	US-09-938-842A-1350	Sequence 1350, Ap
7	424.4	42.6	1237	8	US-10-670-454-7	Sequence 7, Appli
8	418.2	42.0	1403	3	US-09-371-307-64	Sequence 64, Appli
9	418.2	42.0	1403	6	US-10-401-321-64	Sequence 64, Appli
10	388.2	39.0	1390	7	US-10-424-599-21951	Sequence 21951, A
11	381.6	38.3	1008	8	US-10-670-454-9	Sequence 9, Appli
12	356.6	35.8	1318	8	US-10-670-454-5	Sequence 5, Appli
13	354	35.5	984	7	US-10-392-325-3	Sequence 3, Appli
14	354	35.5	1260	7	US-10-437-963-78659	Sequence 78659, A
15	314.2	31.5	1611	8	US-10-425-115-69575	Sequence 69575, A
16	307.8	30.9	783	3	US-09-371-307-67	Sequence 67, Appli
17	307.8	30.9	783	6	US-10-401-321-67	Sequence 67, Appli
18	301.6	30.3	831	7	US-10-425-114-6183	Sequence 6183, Ap
19	285	28.6	927	6	US-10-259-194A-141	Sequence 141, App
20	278.8	28.0	591	7	US-10-424-599-9278	Sequence 9278, Ap
21	272.6	27.4	860	7	US-10-424-599-129307	Sequence 129307,
22	272.6	27.4	860	7	US-10-425-114-7861	Sequence 7861, Ap
23	203.2	20.4	1008	7	US-10-437-963-16086	Sequence 16086, A

ALIGNMENTS

RESULT 1

US-10-821-711-3
; Sequence 3, Application US/10821711
; Publication No. US20040237142A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieger, Elysia K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Wanggen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; FILE OF INVENTION: COMMERCIALY VIABLE TRANSGENIC PLANTS
; FILE REFERENCE: 38-21(52967)B
; CURRENT APPLICATION NUMBER: US/10/821,711
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-10-821-711-3

Query Match	100.0%	Score 996;	DB 8;	Length 999;
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0; Gaps 0;
Matches 996;	Conservative 0;			
Qy	1	ATGGTTGTTCTGTCTCAGCCAGCATTGAACACAGATTTTCTTCTGAAACCACTTCAAGTCC	60	
Db	1	ATGGTTGTTCTGTCTCAGCCAGCATTGAACACAGATTTTCTTCTGAAACCACTTCAAGTCC	60	
Qy	61	ACGCCCTTGTTCAGGGGATTCCTGTGTGTGACCTACGACCCCGATGCCAAGATCTC	120	
Db	61	ACGCCCTTGTTCAGGGGATTCCTGTGTGTGACCTACGACCCCGATGCCAAGATCTC	120	
Qy	121	ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTTCATG	180	
Db	121	ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTTCATG	180	
Qy	181	GAGTTAATGGCAATTTAGAAAACAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	240	
Db	181	GAGTTAATGGCAATTTAGAAAACAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	240	
Qy	241	AAAGACAGAGCTGTGTCGCCCGACCCCTTTCGGCTATGATGACAGAGATTGGCCCAAC	300	
Db	241	AAAGACAGAGCTGTGTCGCCCGACCCCTTTCGGCTATGATGACAGAGATTGGCCCAAC	300	


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QY 301 GGTGATGTCGGTTGGTTCGAATACCTCTCCTCAACACCAACCCCTGATTTATCTCACCC 360
Db 301 GGTGATGTCGGTTGGTTCGAATACCTCTCCTCAACACCAACCCCTGATTTATCTCACCC 360

QY 361 AAATCACTTTGATTTCCGAGAAATCTCATCATTTTCAGGGCGGTGGTGAGAACTAC 420
Db 361 AAATCACTTTGATTTCCGAGAAATCTCATCATTTTCAGGGCGGTGGTGAGAACTAC 420

QY 421 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAATTCATGCGGAGGGTTGGG 480
Db 421 ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAATTCATGCGGAGGGTTGGG 480

QY 481 ATAAGGCAGAGAAATACGTTTAAGCAGTTGCTGAAGGATGAGAAAAGTATTTTCGTGCTTC 540
Db 481 ATAAGGCAGAGAAATACGTTTAAGCAGTTGCTGAAGGATGAGAAAAGTATTTTCGTGCTTC 540

QY 541 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAAATTTGGTTGG 600
Db 541 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAAATTTGGTTGG 600

QY 601 TTGCGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTAACAGCACATCTGGC 660
Db 601 TTGCGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTAACAGCACATCTGGC 660

QY 661 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTT 720
Db 661 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTT 720

QY 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGAATAATGGAGGTTTAAAAAGTGTAAAG 780
Db 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGAATAATGGAGGTTTAAAAAGTGTAAAG 780

QY 781 CATAGGTTTTCGCTGACACAGAGTCAAGTCAAGTTTCAATGATCTACCTTTGGAGGACCA 840
Db 781 CATAGGTTTTCGCTGACACAGAGTCAAGTCAAGTTTCAATGATCTACCTTTGGAGGACCA 840

QY 841 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAGAGGAGGAGTGTG 900
Db 841 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAGAGGAGGAGTGTG 900

QY 901 TACAAAGAGTTCACATGGTGTGAATACAAAGAGGCTGCCTACACTTCAAGGCTAGCTGAT 960
Db 901 TACAAAGAGTTCACATGGTGTGAATACAAAGAGGCTGCCTACACTTCAAGGCTAGCTGAT 960

QY 961 AATAGGCTTGCCTTTCCAGAAATCTGCTGTGAT 996
Db 961 AATAGGCTTGCCTTTCCAGAAATCTGCTGTGAT 996
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RESULT 2

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US-10-670-454-1
; Sequence 1, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
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; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-10-670-454-1

Query Match 100.0%; Score 996; DB 8; Length 1318;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTTGTTCTGCTCAGCCAGCATTTGAACCAAGTTTTTCTTCTGAAACCATTTCAAGTCC 60
Db 68 ATGGTTGTTCTGCTCAGCCAGCATTTGAACCAAGTTTTTCTTCTGAAACCATTTCAAGTCC 127

QY 61 AGCCCTTTGTTTCAACGGGGATTTCTGTTGTCGACCTTCACGCACCCCGATGCCAAGAACTCTC 120
Db 128 AGCCCTTTGTTTCAACGGGGATTTCTGTTGTCGACCTTCACGCACCCCGATGCCAAGAACTCTC 187

QY 121 ATAGTGAACGCGCTGTAGGAGCTTTCGGCTTCTTCAAGCTTTGTGAACCATGTTTCCATTG 180
Db 188 ATAGTGAACGCGCTGTAGGAGCTTTCGGCTTCTTCAAGCTTTGTGAACCATGTTTCCATTG 247

QY 181 GAGTTAATGGCCAAATTTAGAAAACGAGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAG 240
Db 248 GAGTTAATGGCCAAATTTAGAAAACGAGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAG 307

QY 241 AAAGACAGAGCTGTGCTCCCGACCTTTTCGGCTATGTTAGCAAGAGGATTTGSCCCAAAC 300
Db 308 AAAGACAGAGCTGTGCTCCCGACCTTTTCGGCTATGTTAGCAAGAGGATTTGSCCCAAAC 367

QY 301 GGTGATGTCGGTTGGTTCGAATACCTCTCTCTCAACCAACCCCTGATTTATCTCACCC 360
Db 368 GGTGATGTCGGTTGGTTCGAATACCTCTCTCTCAACCAACCCCTGATTTATCTCACCC 427

QY 361 AAATCACTTTGATTTTCCGAGAAATCTCTCATCATTTTCAGGGCGGTGGTGAGAACTAC 420
Db 428 AAATCACTTTGATTTTCCGAGAAATCTCTCATCATTTTCAGGGCGGTGGTGAGAACTAC 487

QY 421 ATTACAGCAGTGAAGAACATGTTGCTATGCGGTGTTTGGAAATGATGGCGAGGGTTGGGG 480
Db 488 ATTACAGCAGTGAAGAACATGTTGCTATGCGGTGTTTGGAAATGATGGCGAGGGTTGGGG 547

QY 481 ATAAGGCAGAGAAATACGTTTAAGCAGGTTTCTGAAGGATGAGAAAAGTATTCGTGCTTC 540
Db 548 ATAAGGCAGAGAAATACGTTTAAGCAGGTTTCTGAAGGATGAGAAAAGTATTCGTGCTTC 607

QY 541 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTCAACCGGAAATTTGGTTGG 600
Db 608 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTCAACCGGAAATTTGGTTGG 667

QY 601 TTTGGGAGGACACAGACCCACAGATAATTTCTGCTTAAAGATCTAAACAGCACATCTGGC 660
Db 668 TTTGGGAGGACACAGACCCACAGATAATTTCTGCTTAAAGATCTAAACAGCACATCTGGC 727

QY 661 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTT 720
Db 728 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTT 787

QY 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTTAATGGAGGTTTAAAAAGTGTAAAG 780
Db 788 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTTAATGGAGGTTTAAAAAGTGTAAAG 847

QY 781 CATAGGTTTTCGCTGACACAGAACTCAAGTTCATGATCTTCAATGATCTTCTTTGGAGGACCA 840
Db 848 CATAGGTTTTCGCTGACACAGAACTCAAGTTCATGATCTTCAATGATCTTCTTTGGAGGACCA 907

QY 841 GCGTTGAGTGAATAATAGCACCTTTTACCTTCAGTGTATGTTAAAGAGGAGGAGTGTG 900
Db 908 GCGTTGAGTGAATAATAGCACCTTTTACCTTCAGTGTATGTTAAAGAGGAGGAGTGTG 967

QY 901 TACAAAGAGTTCACATGGTGTGAATACAAAGAGGCTGCCTACACTTCAAGGCTAGCTGAT 960
Db 968 TACAAAGAGTTCACATGGTGTGAATACAAAGAGGCTGCCTACACTTCAAGGCTAGCTGAT 1027
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QY 961 AATAGGCTTGGCCCTTTCAGAAATCTGCTGCTGAT 996
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Db 1028 AATAGGCTTGGCCCTTTCAGAAATCTGCTGCTGAT 1063
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RESULT 3

US-09-371-307-62
; Sequence 62, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Pillier, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-307-62

Query Match 83.1%; Score 827.4; DB 3; Length 1359;
Best Local Similarity 89.9%; Pred. No. 1.7e-270;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;
QY 1 ATGGTTGTTCTGTCTCAGGAGATTTGAACCAAGTTTCTCTGAAACCAATTCAGTCC 60
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Db 102 ATGGTTGTTCTGTCTCAGGAGATTTGAACCAAGTTTCTCTGAAACCAATTCAGTCC 161
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QY 61 AGCCCTTGTCTCAGGAGATTTCTGTGTGCGACCTCAGCACCCCGATGCCAAGATCTC 120
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Db 162 AGCCCTTGTCTCAGGAGATTTCTGTGTGCGACCTCAGCACCCCGATGCCAAGATCTC 221
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QY 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTCCATTG 180
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Db 222 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTCCATTG 281
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QY 181 GAGTTAATGGCCAAATTAGAAACGAGGCGCTCAGGTTCTTTAAATAATCTCAGTCCGAG 240
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Db 282 CAGTTTCATGGCCAAATTGGAACCGAAACCTCGGGTTCTTCAAAAAACCTCAATCCGAG 341
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QY 241 AAAGACAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTAGCAAGAGGATTCGCCCAAC 300
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Db 342 AAAGACAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTAGCAAGAGGATTCGCCCAAC 401
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QY 301 GGTGATGTGGTTCGAATACCTCTCTCAACACCAACCTGATGTTATCTCACCC 360
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Db 402 GCGATGTGGTTCGAATACCTCTCTCAACACCAACCTGATGTTATCTCACCC 461
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QY 361 AAATCACTTTGCAATTTCCAGAAATCTCTCATATTTTCAGGCGGTGTGAGAACTAC 420
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Db 462 AAGTCACTGTTCAATTTTCAGAAAGTCTCTCAGAAATTTTCAGGCGGTGTGAGAACTAC 521
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QY 421 ATTACAGCTCAAGAACTGCTATGCGGTGTGGAATTCATGCGGAGGGTGGG 480
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Db 522 ATTACAGCTCAAGAACTGCTATGCGGTGTGGAATTCATGCGGAGGGTGGG 581
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QY 481 ATAAGCAGAGAAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAGTATTCGTCCTC 540
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Db 582 ATAAGCAGAGAAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAGTATTCGTCCTC 641
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QY 541 AGTTGAACCACTACCCGCTTGCCTCAGGTCAGGTCAGCACTGAAC---CGGAATTTGGTT 597
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Db 642 AGACTTAACCACTACCCGCCCATGCGCGAGGTGCAAGCAATTGAACGGAAGAAATTTGGTT 701
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QY 598 GGGTTTGGGAGACACACAGACCCACAGATAATTTCTGTCTTTAAGATCTAACAAGCACATCT 657
|||
Db 702 GGAATTTGGAGAGACACACAGACCCACAGATAATTTCTGTCTTTGAGATCTAAACAGCACCTCA 761
|||
QY 658 GGGTTGCAAAATCTGTCTCAGAGATGGCACTTTGGGTTTCAGTCCCACTGATCAGACTTCC 717
|||
Db 762 GGGCTGCAAAATCTGTCTCAGAGATGGCACTTTGGGTTTCAGTCCCACTGATCAAACTTCC 821
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QY 718 TTTTTCATCAATGTTGGTGACGCTCTCAGAGTAAATGACTTAATGCGAGGTTTAAAAAGTGA 777
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Db 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTTAATGCGAGGTTTAAAAAGTGA 881
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QY 778 AAGCATAGGGTTTGGCTTGACACCAACGAAGTCAAGTTTATCAATGATCTACTTTGGAGGA 837
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Db 882 AAGCATAGAGTTTGGCTTGACACCAACGAAGTCAAGTTTATCAATGATCTACTTTGGAGGA 941
|||
QY 838 CAAGCTTGAAGTAAATATATAGCACTTTACCTTCAGTGAATGTTAAAAAGGAGAGATGT 897
|||
Db 942 CCACCTTGTGTGAAAGATAGACCTTTACCTTCAGTGAATGTTAAAAAGGAGAGATGT 1001
|||
QY 898 TTGTACAAAGAGTTTCAATGTTGTAATACAAAGAGGCTGCTACACTTCAAGGCTAGCT 957
|||
Db 1002 TTCTACAAAGAGTTTCAATGTTGTAATACAAAGAGGCTGCTACACTTCAAGGCTAGCT 1061
|||
QY 958 GATAATAGGCTTGGCCCTTTCAGAAATCTGCTGCTGAT 996
|||
Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGAT 1100
|||

RESULT 4

US-10-401-321-62
; Sequence 62, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Pillier, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Baerson, Scott R.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
; FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
; CURRENT APPLICATION NUMBER: US/10/401,321
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-10-401-321-62

Query Match 83.1%; Score 827.4; DB 6; Length 1359;
Best Local Similarity 89.9%; Pred. No. 1.7e-270;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;
QY 1 ATGGTTGTTCTGTCTCAGGAGATTTGAACCAAGTTTCTCTGAAACCAATTCAGTCC 60
|||
Db 102 ATGGTTGTTCTGTCTCAGGAGATTTGAACCAAGTTTCTCTGAAACCAATTCAGTCC 161
|||
QY 61 AGCCCTTGTCTCAGGAGATTTCTGTGTGCGACCTCAGCACCCCGATGCCAAGATCTC 120
|||
Db 162 AGCCCTTGTCTCAGGAGATTTCTGTGTGCGACCTCAGCACCCCGATGCCAAGATCTC 221
|||
QY 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTCCATTG 180
|||
Db 222 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTCCATTG 281
|||

Db 928 TCTCAATCAAAATCTTCTGCTTACAAGCTTAAGCTTGGTGGATTATAGACTTGGTCTCTTT 987
Qy 979 CAGAAA 984
Db 988 GAGAAA 993

RESULT 6

US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1350
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350

Query Match 42.6%; Score 424.4; DB 3; Length 1026;
Best Local Similarity 67.5%; Pred. No. 4.7e-133;
Matches 612; Conservative 0; Mismatches 291; Indels 3; Gaps 1;
Qy 79 ATTCTGTGGTCTGACCTCAGCCACCCGATGCGAAGAAATCTCATAGTGAACGCTGTAGG 138
Db 91 ATCCCGTCGTCAACTAGCCGATCGGAGCGAAACCCGATCTGAAGCCCTGCGAG 150
Qy 139 GACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATTTGAGTTAATGCCCAATTTA 198
Db 151 GAGTTCGGGTTCTTCAAGGTCTGTAACCAACGAGTCCGACCGGAACTCATGACTCGTTA 210
Qy 199 GAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCGCGAGAAACAGAGCTGCTCC 258
Db 211 GAGCAGGAGGCTATTGGCTTCTTCGGCTTTCCTCAGTCTCTTAAAAACCGGCGGTCCA 270
Qy 259 CCGGACCTTTCGGCTATGCTAGCAAGAGGATTGGCCCAACGGGTGATGTCGGTTGGGTC 318
Db 271 CTGAACTGACGTTATGTTGATTAACCGATTGACCAACCGGTGAGCTTGGTTGGAAT 330
Qy 319 GAATACCTCTCTCAACACCAACCTGATGTATCTCACCACCAATCACTTTGCAATTTTC 378
Db 331 GAGTATCTCTCTCAATGCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 390
Qy 379 CGAGAAATCTCATCATTTTCAAGGCGGTGGTGGAGAACTACATTTACAGAGTGAAGAAC 438
Db 391 CGTCAAAACCCCTCAAAATTTTCGCTGAGTGGTGGAGAGTACATGAAGAGATTAAAGAA 450
Qy 439 ATGCTGATGCGGTCTGGAATTTGATGCGGAGGGTGGGGATGAAGCAGAGGAATACG 498
Db 451 GGTGCTCAAGAGTGTGGAGATGTTGCCGAAGAACTAGGGATAGAGCCAGGAGCACT 510
Qy 499 TTAACGAGGTTCTCAAGGATGAGAAAAGTATTCGCTTTCAGGTGTAACCACTACCCG 558
Db 511 CTGAGTAAATGCTGAGAGATGAGAGAGTGAATCTGCTGCTGAGACTAAACCAATTCG 570
Qy 559 CCTTCGCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGTTGGGGAGCACACAGAC 618

Db 571 GC---GGCGAGGAAGAGCGGAGAGATGCTGAAGTGGGGTTTGGGGAACACACAGAC 627
Qy 619 CCACAGATAAATTTCTGCTTAAAGATCTAAACAGCAATCTGGCTTGCAAAATCTGTCTACA 678
Db 628 CCACAGATAAATCTCAGTGTCTAAGATCTAAATACACGCGGGTCTTCAAAATCTGTGTGAAA 687
Qy 679 GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTTTCATCAATGTTGGTGAC 738
Db 688 GATGGAAGTTGGGTCGCTGCTCCCTCTGATCACTCTTCTTCTTCAATTAATGTTGGAGAT 747
Qy 739 GCTCTACAGGTAATGACTAATGAGGAGGTTTAAAGTGTAAAGCATAGGGTTTGGCTGAC 798
Db 748 GCTCTCAGGTTATGACTAAACGAGGTTCAAGAGTGTAAACACACAGGCTCTTACCCGAT 807
Qy 799 ACAACGAGTCAAGGTTATCAATGATCTACTTTTGGAGGACGAGCGTTGAGTGAATAATA 858
Db 808 ACAAGGAGATCGAGGATTTCAATGATATATTTCCGCGGACCGCCATTCAGCCAGAATC 867
Qy 859 GCACCTTACCTTCAGTGTGTTAAAGGAGAGGAGTGTGTGTACAAAGAGTTCACATGG 918
Db 868 GCACCATTTGCCATGCTTGTCCCTTGAGCAAGATGATTGGCTTTACAAAGAAATTCACTTG 927
Qy 919 TGTGAATACAAGAGGCTGCGTACACTTCAAGGCTAGCTGATATAGGCTTGCCCTTTC 978
Db 928 TCTCAATACAATCTTCTGCTTACAAGTCTAAGCTTGGTGAATATAGACTTGGTCTCTTT 987
Qy 979 CAGAAA 984
Db 988 GAGAAA 993

RESULT 7

US-10-670-454-7
; Sequence 7, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-7

Query Match 42.6%; Score 424.4; DB 8; Length 1237;
Best Local Similarity 67.5%; Pred. No. 5.3e-133;
Matches 612; Conservative 0; Mismatches 291; Indels 3; Gaps 1;
Qy 79 ATTCTGTGGTCTGACCTCAGCCACCCGATGCGAAGAAATCTCATAGTGAACGCTGTAGG 138
Db 199 ATCCCGTCGTCAACTAGCCGATCGGAGCGAAACCCGATCTGAAGCCCTGCGAG 258
Qy 139 GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTTGAGTTAATGCCCAATTTA 198
Db 259 GAGTTCGGGTTCTTCAAGGTCTGTAACCAACGAGTCCGACCGGAACTCATGACTCGGTTA 318
Qy 199 GAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGCTCC 258


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Db 319 GAGCAGAGGCTATTGGCTCTTCGGCTTGGCTCAGTCTCTTAAACACGGCCCGGTCCA 378
QY 259 CCGAGCCCTTTTCGGCTATGCTAGCAGAGATTTGGCCCAACCGGTGATCTCGTTGGGTC 318
Db 379 CTTGAACCGTACGGTTATGGTAATAACCGATTGGACCAACGGTACGTTGGTTGATT 438
QY 319 GAATACCTCTCTCTCAACCAACCCCTGATTTATCTCACCCCAATFCATTTGGCATTTTC 378
Db 439 GAGTATCTCTCTCAATCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 498
QY 379 CGAGAAAATCTCATCATTTTACGGCGGTGGTGGAGAACTATATTACAGCATGTAAGAAC 438
Db 499 CGTCAAAACCCCTCAAAATTTTCGGTGAAGTGGTGGAGAGTACATGAAGAGATTAAGGAA 558
QY 439 ATGTGCTATGCGGTGTGGAATTTGATGCGCGAGGGGTTCGGGATAGGCGAGAGGATACG 498
Db 559 GTGTCGTACAAGGTGTGGAGATGGTTCGCCGAAGAACTAGGGATAGAGCAAGGGACACT 618
QY 499 TTAAGCAGGTGTGTAAGGATGAGAAAAGTGAATTCGTGCTTCAGGTGTGAACCACTACCGC 558
Db 619 CTCAGTAAATGCTGAGAGATGAGAAGATGACTCGTGCTGAGACTAAACCATATTCCG 678
QY 559 CTTGCGCCCTGAGGTGCAAGACTGAACCGGAATTTGGTTGGGTTCGGGAGCAGACAGAC 618
Db 679 GC---GGCGGAGGAGAGCGGAGAGATGTTGAAGTGGGGTTTGGGGAACACACAGAC 735
QY 619 CCACAGATAATTTCTGCTTTAAGATCTAACAGCACACTCTGGCTTGCATAATCTGCTCACA 678
Db 736 CCACAGATAATCTCAGTGTCTAAGATCTAATAACACGGCGGGTCTTCAAATCTGTGTGAAA 795
QY 679 GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTTTCAATCAATGTGGTGAC 738
Db 796 GATGGAAGTTGGTCTGCTGCTCCCTGATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 855
QY 739 GCTCTACAGTAAATGACTAATGGAGGTTTAAAGTGAAGCATAGGGTTTGGCTGAC 798
Db 856 GCTCTTTCAAGTTATGACTAAACGGGAGGTTCAAGAGTGTAAACACAGGGTCTTAGCCGAT 915
QY 799 ACACCAAGTCAAGGTTATCAATGATCTACTTTGGAGGACAGCGTTGAGTGAATAATA 858
Db 916 ACAGAGATTCAGAGATTTCAATGATATATTTTCGGCGGACCGCATTTGAGCCAGAGATC 975
QY 859 GCACCTTTTACCTTCAGTGTATGTTAAAGGAGAGGAGTGTGTTGACAAAGATTTCATGG 918
Db 976 GCACCAATGCCATGCTTGTCCCTGAGCAAGATGATTGGCTTTACAAAGATTCACTTGG 1035
QY 919 TGTGAATAACAAGAGCTCGGTACACTTCAAGCTAGCTGATAATAGGCTTGGCCCTTTTC 978
Db 1036 TCTCAATACAAATCTTCTGCTTACAAGTCTAAGCTTGGTGAATTATAGACTTGGTCTCTTT 1095
QY 979 CAGAAA 984
Db 1096 GAGAAA 1101

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RESULT 8

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US-09-371-307-64
; Sequence 64, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10

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; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-371-307-64

Query Match      42.0%; Score 418.2; DB 3; Length 1403;
Best Local Similarity 66.2%; Pred. No. 7.4e-131;
Matches 657; Conservative 0; Mismatches 318; Indels 18; Gaps 3;

QY 1 ATGGTGTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTTTTCTCTCTGAAACCATTCAGATCC 60
Db 149 ATGGTGTGTTCTGTCTCAGCCAGCAACACAGAACTACTCTCTACATCAAGAACTACATGCCA 208
QY 61 AGCCCTTGTTCACGGGGATTTCTGTGTGACCTCAGCACCCCGATGCGCAAGAAATCTTC 120
Db 209 ACGGCATTTCTCTCAACAAATTCCTGTAGTGGACCTCTCCAAACCAAGATGCAAGACCCCTC 268
QY 121 ATAGTGAACGCTGTAGGAGCTTCGCTCTTCAAGCTTGTGAACCATGCTGTCCATTTG 180
Db 269 ATAGTGAAGGCTTGTGAGGAATTTGGAATTTCTTCAAGTCAATCAACCATGGTTCCCATG 328
QY 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTCTCTTTTAAAAAATCTCAGTCCGAG 240
Db 329 GAAACTATATCCCAATTTGGAATCTGAAGCTTTCAAGTTCTCTCTATGCCACTCAATGAG 388
QY 241 AAAGACAGAGCTGTGTCCTCCGACCCCTTTCGGCTATGTAGCAAGAGATTGGCCCAAC 300
Db 389 AAGGAAAAAGTAGGCCCTCCCAACCATATGGGTATGGTAGCAAGAAAATTTGGACACAT 448
QY 301 GGTGATGTGCTGTGGTTCGAATPACCTCTCTCAACACCAACCCCTGATGTTATCTCACCC 360
Db 449 GGGGATGTGGTGTGGTTGAGTACCTTCTTCAACACCAATCAAGAACACAACT----- 503
QY 361 AAATCACTTTGCAATTTCCGAGAAAATCTCATCATTTTCAGGGCGGTGGTGAGAACTAC 420
Db 504 -----TCTCTGTTTATGGCAAAAACGCTGAGAAAATTTAGGTGTTGTTGTAACAGTTAC 556
QY 421 ATTACAGCATGTAAGAACATGTGCTATGCGGTGTGGAAATGATGCGGAGGGGTGGG 480
Db 557 ATGTCTTCTGTGAGGAAAAATGGCATGTGAGATTTCTTGAGCTGATGGCAGAGGATTTGAAG 616
QY 481 ATAAGCAGAGCAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTC 540
Db 617 ATCAACAAAAAATGTGTTTAGCAAGCTTCTTATGATTAAGAGAGTGAATCTGTGTTTT 676
QY 541 AGGTTGAACCACTACCCGCTTTCGCTGAGGTGCAAGCACTGAACCGGAAATTTGGTTGGG 600
Db 677 AGGGTGAATCACTACCTGCTTTCGCTGAACTT---GTGAATGGTCAAAAACATGATAGGG 733
QY 601 TTTGGGGAGACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAAACAGCACTGTGCG 660
Db 734 TTTGGAGAAACACACGAGCCCAAAAATCATTTCTCTACTTAGGTCCAACAAATACTTCAGGC 793
QY 661 TTGCAAAATCTGTCTCAGATGCGACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTT 720
Db 794 CTTCAAGATTTTCTTAGAGATGAAACTGGATTTCACTCCCACTGATCAAAATCTTTC 853
QY 721 TTCAATCAATTTGGTGACGCTCTACAGGTAATGACTAATTTGGAGGTTTAAAAAGTGAAG 780
Db 854 TTTCAAAATTTGGTGATTTCTCTTCAAGTTATGACCAATTTGAAAGGTTTCGAAAGTGTGAAA 913
QY 781 CATAGGTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCA 840
Db 914 CACAGAGTTTTCGACAAATGGATTTAAGTCTAGACTCTCAATGATTTACTTTTGGAGTCCA 973
QY 841 GGGTTGAGTGAATAATATAGCACTTTTACCTTCAGTGTGATGTTTAAAAAGAGAGAGGTTTGG 900
Db 974 CATTGAGTGAAGAAATAGTACATTTCTTCACTTATG---AAAGGAAAAAGAGCTTA 1030
QY 901 TACAAAGAGTTTCATGTTGTGAATACAAAGAGGCTGGGTACACTTCAAGGCTAGCTGAT 960

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Db 1031 TACAAAGAGTTTACGGTTCAGTATATAAAATTTAAACCTATGCTTCAAGATTGGCTGAT 1090
 Qy 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCT 993
 Db 1091 AATAGGCTTGGACATTTTGAGAGATTGTTGCT 1123

RESULT 9

US-10-401-321-64
 ; Sequence 64, Application US/10401321
 ; Publication No. US20030233679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Sherri M.
 ; APPLICANT: Heck, Gregory R.
 ; APPLICANT: Pillier, Kenneth J.
 ; APPLICANT: Kilshore, Ganesh M.
 ; APPLICANT: Ellich, Tedd D.
 ; APPLICANT: Logusch, Eugene W.
 ; APPLICANT: Rao, Sudabathula
 ; APPLICANT: Ream, Joel E.
 ; APPLICANT: Logusch, Sherry J.
 ; APPLICANT: Baerson, Scott R.
 ; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
 ; FILE REFERENCE: 11899.0216.DVUS01 (MOB:216--1)
 ; CURRENT APPLICATION NUMBER: US/10/401,321
 ; CURRENT FILING DATE: 2003-03-27
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 64
 ; LENGTH: 1403
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-10-401-321-64

Query Match 42.0%; Score 418.2; DB 6; Length 1403;
 Best Local Similarity 66.2%; Pred. No. 7.4e-131;
 Matches 657; Conservative 0; Mismatches 318; Indels 18; Gaps 3;
 Qy 1 ATGGTTGTTCTCTCTCAGCAGCATTTGAACCAAGTTTTCCTTCTGAAACCACTTCAAGTCC 60
 Db 149 ATGGTTGTTCTCTCAGCAGCATTTGAACCAAGTTTTCCTTCTGAAACCACTTCAAGTCC 208
 Qy 61 AGCCCTTGTTCACGGGGATTCCTGTGTCGACCTCAGCAGCCCGATGCCAAGAAATCTC 120
 Db 209 AGCGCATTCCTCAACAATTCCTGTGTCGACCTTCCAAACCAAGATGCAAGACCTTC 268
 Qy 121 ATAGTGAAGCCTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTCCATG 180
 Db 269 ATAGTGAAGCCTGTGAGGAATTTGGATTTCTTCAAAAGTCATCAACCATGGTGTCCCATG 328
 Qy 181 GAGTTAATGGCCAAATTTAGAAACGAGCCCTCAGGTCTTTTAAATAATCTCAGTCCGAG 240
 Db 329 GAAATATATCCAAATTTGAATCTCAAGCTTCAAGTCTTCTCTATGCCACTCAATGAG 388
 Qy 241 AAAGACAGAGCTGTGTCCTCCCGACCTTTCGGCTATGTTAGCAGAGGATTTGGCCCAAC 300
 Db 389 AAGGAAAAGTAGGCGCTCCCAACCATATGTTGTTAGTGAAGAAATTTGGACAAAT 448
 Qy 301 GGTGATGTCGGTGGTGGTGAATACCTCTCTCAACAACCAACCTGTATTTATCTCAACC 360
 Db 449 GGGGATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 503
 Qy 361 AAATCACTTTCATTTTCGAGAAATCTCTATCATTTTCAGGCGGTGGTGGAGAACTAC 420
 Db 504 -----TCTGTTTATGGCAAAACCGTGAATAATTTAGGTGTTGTTGAACAGTTAC 556
 Qy 421 ATTACAGCAGTGAAGAAATATGTGCTATGCGGTGTTGGAATTTGATGCGGAGGGTGGG 480
 Db 557 ATGCTTCTGTGAGGAAATGTCATGTGAGATTTCTTGAGTGTGATGCGGAGGAAATTTGAG 616
 Qy 481 ATAAGGACAGGAATACGTTAAGCAGGTTGCTGAAAGGATGAGAAAGGATTCGTGCTTC 540

Db 617 ATACAAACAAAAATGTGTTTAGCAAGCTTCTTATGGATAAAGAGAGTGACTCTCTTTT 676
 Qy 541 AGGTTGAACCACTACCCCGCTTGCCTGAGTGCAGCACTGAACCCGAAATTTGTTGG 600
 Db 677 AGGTTGAATCACTACCTGCTTGCCTGAACTT---GTGAATGGTCAAAACATGATAGG 733
 Qy 601 TTTGGGAGACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAAACAGCATCTGGC 660
 Db 734 TTTGGAGAACACACGGACCCCAAAATCATTTCTTACTTAGGTCCAAATACTTTCAGGC 793
 Qy 661 TTGCAAAATCTGCTCACAGATGGCACTTTGGTTTTCAGTCCCACTGATCAGACTTCTTT 720
 Db 794 CTTCAATTTTCTTAGAGATGGAACTGGATTTTCAGTCCCACTGATCAGAAATCTTTC 853
 Qy 721 TTTCAATTTTGTGTGACGCTCTACAGGTAATGACTAATGGAGGTTTAAAAGTGTAAAG 780
 Db 854 TTTCAATTTTGTGTGATTTCTTTCAGGTTATGACCAATGGAGTTTTCGAAGTGTGAA 913
 Qy 781 CATAGGTTTGTGGTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTGGAGGACA 840
 Db 914 CACAGAGTTTGGACAAATGGATTTAAGTCTAGACTCTCAATGATTTACTTTGGAGGTCCA 973
 Qy 841 CGGTTGAGTGAATAATATAGCACCTTTACCTTTCAGTGTATTAAGAGGAGAGGAGTGTG 900
 Db 974 CCAATTTGAGTGAATAATATAGTACCATTTATCTTCACTTATG---AAAGGAAAAAGCTTA 1030
 Qy 901 TACAAAGAGTTTCAATGCTGTGAATACAAAGAGGCTGCTACACTTCAAGGCTAGCTGAT 960
 Db 1031 TACAAAGAGTTTACGTTGCGAGTATAAAATTTAACTATGCTTCAAGATTGGCTGAT 1090
 Qy 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTCT 993
 Db 1091 AATAGGCTTGGACATTTTGGAGAAATTTGTTGCT 1123

RESULT 10

US-10-424-599-21951
 ; Sequence 21951, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kowalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 21951
 ; LENGTH: 1390
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_119826C.1
 US-10-424-599-21951

Query Match 39.0%; Score 388.2; DB 7; Length 1390;
 Best Local Similarity 64.1%; Pred. No. 1.3e-120;
 Matches 637; Conservative 0; Mismatches 343; Indels 13; Gaps 3;
 Qy 1 ATGGTTGTTCTGCTCAGCAGCATTTGACCAAGTTTTCCTTCTGAAACCACTTCAAGTCC 60
 Db 175 ATGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 234
 Qy 61 ACGCCCTTGTTCAGGGGATTCCTGTGTGCTCAGCTCAGCAGCCCGATGCCAAGAAATCTC 120
 Db 235 ACTGCATTCCTCAACAATTTCCCATAGTGAACCTCTCAACCTGATGCAAGACCTT 294
 Qy 121 ATAGTGAAGCCTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTTCCATTG 180
 Db 295 ATAGTGAAGCCTGTGAGGAGTTTGGATTTCTTCAAAAGTCATCAACCACTGGTGTCCCAT 354

QY 919 TGTGAATACAAAGGCTCGTACACTTCAAGGCTAGCTGATTAATAGGTTGCCCTTTC 978
Db 913 TCTCAATACAAAGTTATCTGCTTACAAAATAAGCTTGGTGACTATATAGGCTTGGTCTCTTT 972
QY 979 CAGAAA 984
Db 973 GAGAAA 978

RESULT 12
US-10-670-454-5
; Sequence 5, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.097000
; CURRENT APPLICATION NUMBER: US/10/670,454
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1243, 1265)
; OTHER INFORMATION: unidentified residue
US-10-670-454-5

Query Match 35.8%; Score 356.6; DB 8; Length 1318;
Best Local Similarity 63.2%; Pred. No. 7.5e-110;
Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;

QY 65 CCTGTGTTACGGGGATTCTCTGTGGTGCAGCTCAACGACCCCGATGCGAAGATCTCATAG 124
Db 78 CCGGTTCTCTAATCCGGTTATAGATATGTCTGACCCAGATCCAAACATGCGCTCG 137

QY 125 TGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTCATTTGGAGT 184
Db 138 TGAAGCATGCGAAGACTTCGGCTTCTTCAAGGTGATCAACCATGCGGTTCGCGAGAGC 197

QY 185 TAAATGCCAATTTAGAAACGAGGCGCTCAGCTTCTTTAAAAATCTCAGTCCGAGAAG 244
Db 198 TAGTCTCTGTTTGAACACGAGCGTGCATTTCTCTCTGTTGCCCAAGTCAGAGAAA 257

QY 245 ACAGAGCTGTTCCCGGCTATCTGCTGCTAGCAAGAGGATTGCGCCCAACGGTG 304
Db 258 CCAAGTCG---CAGGTATCCCTTCGGATACGGAAACAGTAAGATTGTCGGAATGGTG 314

QY 305 ATGTGCGTTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCCAAT 364
Db 315 ACGTGGTTGGGTGAGTACTTGTGTGATGAACGCTAATCATGATTCGGGTTCGGGTCCAC 374

QY 365 CACTTTGCATTTTCGAGAAAATCTCATCATTTTCAAGGCGGTGGTGGAGAACTACATTA 424
Db 375 TATTTCCAGTCTTCTCAAAAGCCCGGAACTTTTCAGAAACGCAATTTGGAAGAGTACAAA 434

QY 425 CAGCAGTAGAACACATGCTATCGGTGTTGCAATTTGATGCGGAGGGGTTGGGGATAA 484
Db 435 CATCAGTAGAAGAAAATGCAATTCGATGTTTGGAGAAAGATCAGATGGGCTAGGGATCA 494

QY 485 GCGAGAGGAATACGTTAAGCAGGTTTCTGAAGGATGAGAAAGATGATTCGTGCTTCAGGT 544
Db 495 AACCGAGAACACACTTAGCAAGCTTGTGTCTGACCAAAACACCGGACTCGATATTGAGAC 554
QY 545 TGAACCACTACCGCTTGGCCCTGAGGTGCAAGCACTGAAC-----CGAATTTGG 595
Db 555 TTAATCACTATCCACCATGTCTCTTAGCAATAGAAAACCAATGGTGGTAAGAAATGGA 614
QY 596 TTGGGTTTGGGAGCACACAGACCCACAGATAAATTTCTGTCTTAAGATCTAACACACAT 655
Db 615 TTGGTTTGGTGAACACACAGATCTCTCAATCATCTCTGTCTTAAGATCTAACACACTT 674
QY 656 CTGGCTTCCAAATCTGTCTCAGATGCGACTTGGGTTTTCAGTCCCACTGATCAGACTT 715
Db 675 CTGGTCTCCAAATTAATCTAAATGATGGCTCATGGATCTGTCTCCCTCCCGATCACACTT 734
QY 716 CTTTTTTCATCAATGTTGGTGACGCTCTACAGGTAAATGACTAAATGGGAGTTTAAAAAGTG 775
Db 735 CTTCTTCTTCAACGTTGGTGACTCTCTCAGGTGATGACAAATGGGAGGTTCAAGAGCG 794
QY 776 TAAAGCATAGGTTTGGCTGACACACAAAGTCAAGGTTATCAATGATCTACTTTGGAG 835
Db 795 TGAGGCATAGGTTTGTAGCTAACTGTAATAAATACTAGGGTTTCTATGATTTACTTTCGCTG 854
QY 836 GACCAAGCTTGAAGTAAATATAGCACTTTACCTTTCAGTGATGTTAAAGAGAGGAGT 895
Db 855 GACCTTCATTCAGTCAAGAAATCGCTCCGTTGACATGTTTGTATAGACAATGAGGACGAGA 914
QY 896 GTTTGTACAAAGAGTTTCAATGTTGTAATACAAAGGCTGCGTACACTTCAAGGCTAG 955
Db 915 GTTGTACGAGAGTTTACTTGGTCTGAATACAAAACACTTACCTACCACTCTAGATTGT 974
QY 956 CTGATAATAGGCTTGCCCTTTTCCAGA 982
Db 975 CTGATAATAGGCTTCAACAATTCGAAA 1001

RESULT 13
US-10-392-325-3
; Sequence 3, Application US/10392325
; Publication No. US20040060080A1
; GENERAL INFORMATION:
; APPLICANT: Tanaka, Hiroshi
; APPLICANT: Kayano, Toshiaki
; APPLICANT: Matsuoka, Makoto
; APPLICANT: Kobayashi, Masatomo
; APPLICANT: Saito, Tamio
; APPLICANT: Sakamoto, Tomoaki
; APPLICANT: Sakai, Miho
; TITLE OF INVENTION: GIBBERELLIN 2-OXIDASE GENE, FUNCTIONS AND USES THEREOF
; FILE REFERENCE: SH2-014
; CURRENT APPLICATION NUMBER: US/10/392,325
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 7
; PRIOR APPLICATION NUMBER: JP 2002-276051
; PRIOR FILING DATE: 2002-09-20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
; OTHER INFORMATION:
US-10-392-325-3

Query Match 35.5%; Score 354; DB 7; Length 984;
Best Local Similarity 60.9%; Pred. No. 4.8e-109;
Matches 598; Conservative 0; Mismatches 375; Indels 9; Gaps 1;

QY 2 TGGTTGTTCTGTCTCAGCGCAGCAATTTGAACCGAGTTTTCCTTCTTGAAACCACTCAAGTCCA 61

Db 5 TGGTTCTCGTGGCCGCCCGCTCGATCATACCCCGTGTGAGGTGCGCGGACCCCG 64
Qy 62 CGCCCTTGTTCAGGGGATTTCTGTGTCGACCTCAGCACCCCGGATGCCAAGATCTCA 121
Db 65 GCGACGTCTTCTCCGCGGTGCGGTCTGAGCTCTGGGAGCCCGCGCGGAGGGCGG 124
Qy 122 TAGTGAACCCCTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTTCCATTGG 181
Db 125 TGGTGACGCCCTGCGAGCGGTACGGGTCTTCAAGGTGTCACACACGCGGTGGCCACGG 184
Qy 182 AGTTAATGCGCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCGAGA 241
Db 185 ACACGATGACAAAGCGGAGTCGGAGCGGTCTCAGGTTCTTCTCCACAGCGACGCCGACA 244
Qy 242 AAGACAGAGCTGTCTCCCGCCCGCCCTTTCGGCTATGTTAGCAAGAGATTGGCCCAAGC 301
Db 245 AGACCGCTTCCGCGCGGCTTACCGGTTCCGGTACGCGAGCAAGCGGATCGGGTTCAATG 304
Qy 302 GTGATGTCGGTTGGGTGCAATACCTCTCTCTCAACACCAACCCCTGATGTTATCTCACCCA 361
Db 305 GCGACATGGGTGGCTCGAGTACCTCTCTCGCCCTCGACGACGCGTCTGCGCGAGC 364
Qy 362 AATCATTTGGCAATTTCCGAGAAAATCTCTCATCATTTTCAGGGGGTGTGGAGAACTACA 421
Db 365 CTTGCACCGTCCCGTCTCTCGC-----CGGTCTTCCGGGCGGTCTCTGAACGAGTACA 415
Qy 422 TTACAGCAGTGAACATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGTTGGGA 481
Db 416 TCTCGGGGTGCGGAAGGTGGCGGTGCGGGTGTATGAGGCGATGTCCGAGGGGCTGGGA 475
Qy 482 TAAGGACAGAGGAATACGTTAAAGCAGGTGTCTGAAGGATGAGAAAAGTATGTTGTTTCA 541
Db 476 TTGCGCAGCGCGACGCGCTGAGCGCGCTGTGACGCGGAGGAGCGACAGGTCTTCC 535
Qy 542 GGTGAACCACTACCCCGCTTGCCTTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGT 601
Db 536 GGTGAACCACTACCCCGCTGCGCGCGCTGCGAGGGGCTCGGCTGCAAGCGTCAACGGCT 595
Qy 602 TTGGGAGACACAGACCCACAGATAATTTCTGCTTTAAGATCTAACACACATCTGGCT 661
Db 596 TCGCGAGACACACGACCCGAGCTCGTCTCGGTGCTCCGCTCAACCGCACGTCGCGCC 655
Qy 662 TGCAATCTGTCTCAAGATGGCACCTTGGGTTTCAGTCCCACTCTGATCAGACTTCCTTTT 721
Db 656 TGCAGATCGGCTCCGCGACGCGCAGTGGGTGTCGTCGCCCTCCGACCGGACTCTCTCT 715
Qy 722 TCATCAATGTTGGTACGCTCTACAGGTAAATGACTAATGGGAGTTTAAAGTGTAAAGC 781
Db 716 TCGTCAACGTTCGGCGACTCGTTGACGGTTCTGACCAATGGGAGGTTCAAGAGCGTGAAGC 775
Qy 782 ATAGGGTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCA 841
Db 776 ACAGGGTGGTGGCCAAACAGCTTAAAGTCTAGGGTTTCTTCACTTTGAGGGGCCAC 835
Qy 842 CGTTGAGTGAAAATATAGCACCTTTTACCTTTCAGTGTATGTTTAAAGGAGAGGAGTGTTC 901
Db 836 CGTTACCAACAGAGGATTCACCAATTCACACGCTGCTGGGGGAGGAGACAGGCTGT 895
Qy 902 ACAAGAGTTACATGGTGTGAATACAAGAAGCTCGGTACACTTCAAGGCTAGCTGATA 961
Db 896 ACAAGAGTTACATGGGATGAGTACAAGAAGCTCGCTACAAATCAAGGCTTGGAGACA 955
Qy 962 ATAGGCTTGCCTTTCCGAA 983
Db 956 ACAGGCTGGCCCGAGTTTGAA 977

RESULT 14

US-10-437-963-78659

; Sequence 78659, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 78659
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78444C.1
US-10-437-963-78659

Query Match 35.5%; Score 354; DB 7; Length 1260;

Best Local Similarity 60.9%; Pred. No. 5.6e-109; Mismatches 375; Indels 9; Gaps 1;

Matches 598; Conservative 0; Mismatches 375; Indels 9; Gaps 1;

Qy 2 TGGTTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTCCTCTCTGAAACCATTTCAAGTTCCA 61
Db 144 TGGTTCTCGTGGCCCGCCGCGCTCGATCATATCCCGTGTGTAGGTGCGCGGACCCCG 203
Qy 62 CGCCCTTGTTCACGGGATTCCTGTGGTCGACCTCAGCACCCCGATGCCAAGAATCTCA 121
Db 204 GCGACGTCTTCTCCGCGGTGCGGTGCTCGACCTCGGAGACCCCGCGCGGAGGGCGG 263
Qy 122 TAGTGAACCCCTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTTCCATTGG 181
Db 264 TGGTGACGCTTCTCAGCGGTACGCGGTCTTCAAGGTGTCACACCGCGGTGGCCACGG 323
Qy 182 AGTTAATGCGCAATTTAGAAAACGAGGGCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGA 241
Db 324 ACACGATGGACAAAGCCGAGTCGGAGGCGCTCAGGTTCTTCTCCAGACGACGCGCGACA 383
Qy 242 AAGACAGAGCTGGTCCCGCCCGACCTTTCGGGTATGTTAGTGAAGAGGATTTGGCCCAAGC 301
Db 384 AGGACCGTTCGCGCGCGCTACCGGTTCCGGGTACGCGAGCAAGCGGATCGGGTTCAATG 443
Qy 302 GTGATGTCGGTTGGTTCGAATACCTCCTCAACACCAACCTCGATGTTATCTCACCCA 361
Db 444 GCGACATGGGTGGGTTCGAGTACCTCTCTCGCCCTCGACGACGCGTCTGCGCGAGC 503
Qy 362 AATCACTTTTCCGAGAAAATCTCTCATCATTTTCAGGGCGGTGGTGGAGAACTACA 421
Db 504 CTTGCACCGTCCGCTCTGCG-----CGGTCTTCCGGGCGCTCTGACGAGTACA 554
Qy 422 TTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGTTGGGA 481
Db 555 TCTCGGGGTGCGGAAGGTGGCGGTGATGGAGCGATGTCCGAGGGGCTGGGA 614
Qy 482 TAAGCAGAGGAATAGTTAAGCAGGTTCTGAAAGATGAGAAAAGTATGTTGTTGTTGGT 541
Db 615 TTGCGCAGCGGACGCGCTGAGCGGTGTTGACGCGGAAGGAGCGACCGAGGTGTTCC 674
Qy 542 GGTGAACCACTTACCCGCTTCCCTTGAGGTGCAAGCACTGAAACCGGAATTTGGTTGGGT 601
Db 675 GGTGAACCACTTACCCGCTGCGCGCGCTGACGGGCTCGGTGACGCGTCAACGGCT 734
Qy 602 TTGGGAGACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAACAGCAATCTGGCT 661
Db 735 TCGGGAGACACCGACCCGAGCTCTCTCGGTGCTCCGCTCAAAACGCGAGCTCGCGCC 794
Qy 662 TGCNAATCTGTCTCAGATGCGACTTGGGTTTTCAGTCCCACTGATCAGACTTCCTTTT 721
Db 795 TGCAGATCGGCTCCGCGACGCGCAGTGGGTGTCCGTGCTCTCCGACCGCGACTCTCTT 854

QY 722 TCATCAATGTTGGTACCGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAGC 781
Db 855 TCGTCAACGTCGCGGACTCGTTGTCAGAGTTCTGACCAATGGGAGGTTCAAGAGCGTGAAGC 914
QY 782 ATAGGGTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAAG 841
Db 915 ACAGGGTGTGGCCAAACAGCCTAAAGTCTAGGGTTTCTTCAATCTACTTTGGAGGGCCAC 974
QY 842 CGTTGAGTGAANAATATAGCACCTTTACCTTTCAGTGTATGTTAAAGGAGGAGGAGTGTGT 901
Db 975 CGTTAGCAGAGGATTCACCATTTGCCACAGCTGCTGGGGGAGGAGCAGAGCGCTGT 1034
QY 902 ACAAGAGTTTCAATGCTGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCTGATA 961
Db 1035 ACAAGGAGTTTCAATGGGATGATGTAAGAAGGCTGCCTTACAAATCAAGGCTTGGAGACA 1094
QY 962 ATAGGCTTGCCCTTTCCAGAA 983
Db 1095 ACAGGCTGGCCAGTTTGAA 1116

RESULT 15

US-10-425-115-69575
; Sequence 69575, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 69575
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MR14577_163444C.1
US-10-425-115-69575

Query Match 31.5%; Score 314.2; DB 8; Length 1611;
Best Local Similarity 59.3%; Pred. No. 2.5e-95;
Matches 576; Conservative 0; Mismatches 383; Indels 12; Gaps 2;

QY 16 CAGCAGCATTTGAACAGATTTTCTTCTGAAACCATTCAGTCCACGCCCTTGTTCAG 75
Db 193 CGGCCTGTCTGACAGATCCGCTCTCTGCGGTCCCGGGCCCGGAGGACAGCTTCTCG 252
QY 76 GGGATTCGTGTCGACCTCAGCACCCGATGCCAAGATCTCATAGTGAACGCTGT 135
Db 253 GGAGTGCCCGTCTGACCTGTCTCAGCACGCGCGCGCGGCGATCTCGACCGCTGC 312
QY 136 AGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTGTCTTCCATTGGAGTTAATGGCCAA 195
Db 313 GAGCGCTTCGGGTTCTTCAAGTGTCTCAACACGCGGTGCGCGGCCACCATGGACAGG 372
QY 196 TTAGAAAACGAGGCCCTCAGGTTCTTTTAAATAATCTCAGTCCGAGAAAGACAGAGTGT 255
Db 373 GCGAGTCCGAGGCGCTCAGGTTCTTTCGCGAGGCGCAGCGCGGACAAGGACCGCGCGGG 432
QY 256 CCCCCGACCTTTCGGCTATGGTAGAGAGGTTGGCCAAACGGTGTATGTCGGTTGG 315
Db 433 CCGGCGTACCTCTCTCGGGTACGCGAGAGCGGATCGGGCTCAATGGCGACATGGGGTGG 492
QY 316 GTCGAATACCTCTCTCAACACCAACCTGTATGTTATCTCACCCAAATCACTTTGCATT 375
Db 493 CTCGAGTACTCTCTCTCGCGTGCAGCGCGGTGCTCTCCGAGCGCTGCCCGTGGCC 552
QY 376 TTCCGAGAAAATCCTCATCTTTCAGGGCGGTGGTGGAGAACTACATTTACAGCAGTGAAG 435

Db 553 TCCAGCG-----CGCGCTTCGGAGCCGCTGAACGAGTAGCTCGCGCCGTGGG 603
QY 436 AACATGTCTATGCGGTGTTGGAATTTGATGCGGAGGGGTTGGGATTAAGGCAGAGGAAT 495
Db 604 AAGGTGGCGCGCGTGTGCTGAGGCGGATGCGGAGGSCCTGGGCATTTCGCGACCGGAC 663
QY 496 AGTTAAGCAGGTTGCTGAAAGATGAGAAAGTATGTTCTGCTTCAGGTTGACACACTAC 555
Db 664 CGCTGAGCTCCATGTTGAGCGCGCGGAGCGACCAAGGTGTTCCGCGTGAACCACTAC 723
QY 556 CGCCTTCGCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGTTGGGAGCACACA 615
Db 724 CGCCTTCGCCCGCGCTGCAGGGCTTGGGCTGCGAGCGCCACGCGCTTCGCGAGCACACC 783
QY 616 GACCCACAGATAAATTTCTGCTCTTAAGATCTAACAGCACATCTGGCTTGCATAATCTGTCT 675
Db 784 GACCGCAGATCATCTCGTGTCTCGCTCCAAACGCGACCTCGGCTTCAGATCGCGCTC 843
QY 676 ACAGATGGCAC---TTGGGTTTCAGTCCACCTGATCAGACTTCTTTTTCATCATGTT 732
Db 844 CGCGACGGCGGCGAGTGGGTCTCGGTGCCCTCCGACCGCGACGCGCTTCTTCTTAACGTC 903
QY 733 GGTGACGCTCTACAGGTAATGACTAATGCGAGGTTTAAAGTGTAAAGCATAGGCTTTTG 792
Db 904 GCGGACTCGTTGCGAGGTCTGACCAACGCGGAGGTTTCAGGAGCGTGAAGCACCGGGTGGT 963
QY 793 GCTGACACACAGAAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCGAGCGTTGAGTGA 852
Db 964 ACCAACGCTCAAGTCCAGAGTTTCTTCTACTTTCGCGGGCGCGCGCTGGGCGAG 1023
QY 853 AATATAGCACCTTTACCTTTCAGTGTATGTTAAAGGAGAGGAGTGTGTTGTACAAAGATT 912
Db 1024 CGGATCGCGCGCTGCGCGAGGTGCTGCGGAGGAGGAGAGAGCTGTGTACAAAGAGTTC 1083
QY 913 ACATGTTGTGAATACAAGAGGCTGCGTACACTTCAAGSCTAGCTGATAATAGGCTTGCC 972
Db 1084 ACGTGGGCGAGTAGTACAAGAGGCGCGGTACAGAGCGGCTCGCGGACAAACAGGCTGGCC 1143
QY 973 CTTTTCAGAA 983
Db 1144 CAGTTTGAA 1154

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Job time : 939.171 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 18:17:41 ; Search time 179.487 Seconds
(without alignments)
2879.764 Million cell updates/sec

Title: US-10-670-454-1_COPY_68_1063

Perfect score: 996

Sequence: 1 atggtgtgtctgtctcagcc.....tccagaaaatctgtctgat 996

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

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10: /cgn2_6/ptodata/2/pubpna/US60 NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56.4	5.7	1017	7	US-11-152-892-5
2	40	4.0	1011	7	US-11-152-892-3
3	39.2	3.9	3861	7	US-11-152-892-2
C 4	38.8	3.9	150437	7	US-11-112-908-44
C 5	38.8	3.9	182314	7	US-11-112-908-45
6	36	3.6	2171	7	US-11-152-892-1
7	35	3.5	3770	7	US-11-174-166-19
8	33.2	3.3	611587	7	US-11-117-187-209
C 9	33	3.3	921	7	US-11-112-908-140
C 10	33	3.3	180862	7	US-11-112-908-40
C 11	32.2	3.2	163317	7	US-11-117-187-212
C 12	31.6	3.2	1138	6	US-10-750-185-56890
C 13	31.6	3.2	101786	7	US-11-117-187-199
14	31.4	3.2	167116	7	US-11-121-086-44
C 15	31.4	3.2	187786	6	US-10-995-561-13474
C 16	31.4	3.2	187986	6	US-10-995-561-13252
17	31.2	3.1	1596	6	US-10-750-185-49342
18	31.2	3.1	2701	6	US-10-750-185-58921
19	31	3.1	1866	6	US-10-750-185-59097
C 20	31	3.1	3109	6	US-10-750-185-45757
C 21	31	3.1	193363	7	US-11-112-908-32
22	31	3.1	380749	6	US-10-995-561-13216
23	30.8	3.1	1464	6	US-10-750-185-27149

24	30.8	3.1	1595	6	US-10-750-185-34358
25	30.8	3.1	4173	7	US-11-063-343-16
26	30.8	3.1	241805	6	US-10-995-561-13215
27	30.6	3.1	868	6	US-10-750-185-50973
C 28	30.4	3.1	987	6	US-10-750-185-44904
C 29	30.4	3.1	1898	6	US-10-750-185-34003
C 30	30.4	3.1	2761	6	US-10-995-561-238
C 31	30.4	3.1	2911	6	US-10-750-185-31364
C 32	30.4	3.1	43943	6	US-10-995-561-13466
C 33	30.4	3.1	96539	6	US-10-995-561-13289
34	30.4	3.1	101001	6	US-10-995-561-13255
35	30.4	3.1	173995	6	US-10-995-561-13277
C 36	30.2	3.0	1788	6	US-10-750-185-51119
C 37	30.2	3.0	2639	6	US-10-750-185-53993
C 38	30.2	3.0	135019	6	US-10-849-438-11
C 39	30.2	3.0	150468	7	US-11-112-908-56
C 40	30.2	3.0	193789	7	US-11-112-908-55
41	30	3.0	12756	6	US-10-995-561-13434
C 42	30	3.0	96539	6	US-10-995-561-13289
C 43	30	3.0	200628	7	US-11-121-086-62
C 44	30	3.0	1125000	6	US-10-995-561-13286
C 45	29.8	3.0	755	6	US-10-750-185-32477

ALIGNMENTS

RESULT 1

US-11-152-892-5
; Sequence 5, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1014)
US-11-152-892-5

Query Match	5.7%	Score 56.4;	DB 7;	Length 1017;
Best Local Similarity	55.7%	Pred. No. 4.6e-09;		
Matches 108;	Conservative	0;	Mismatches 86;	Indels 0;
Gaps	0;			
Qy	674	TCACAGTGGCACTGGGTTTCAGTCCACCTGATCAGACTTCCTTTTCATCAATGTTG	733	
Db	704	TCAAAGACAATAGATGGATCGCTGTAAACCTTAATCCTAAAGCTCTCATATCAATATTG	763	
Qy	734	GTGACGCTCTACAGGTAATGACTAATGGAGGTTTAAAGTGTAAAGCATAGGTTTTCG	793	
Db	764	GTGACTTATTTCAGCATGGAGCATGGCATGTACAAAGTGTGACACCGTGTGATCA	823	
Qy	794	CTGACACACGAAGTCAAGTTTATCAATGATCTACTTTGGAGGACACGGTTGAGTGA	853	
Db	824	CGAACCCAAAGGTGAGAGATTCTCAACGGCTTATTATTGTGTCATCATACGACGCG	883	
Qy	854	ATATAGACCTTTA	867	
Db	884	TTATAGATGTTCA	897	

Qy 112 AAGAACTCATAGTGAACGGCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGT 171


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; LENGTH: 182314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-45

Query Match      3.9%; Score 38.8; DB 7; Length 182314;
Best Local Similarity 58.8%; Pred. No. 0.24;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 769 AAAAGTGAAGCATAGAGGTTTGGCTGACACAAAGTCAAGGTATCAATGATCTAC 828
DB 65032 ACAAATAAAGCAAGAGGTGTAGTGTATCAAAATCAATCAATTTTACAGTATGAT 64973

QY 829 TTTGAGGACCAAGCGTGTAGTGAATAATATAGCACCTTTACCTTTCAGTGTGTTA 882
DB 64972 GATTTAGGAGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 64919

RESULT 6
US-11-152-892-1
; Sequence 1, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2171
; TYPE: DNA
; ORGANISM: Arabidopsis
US-11-152-892-1

Query Match      3.6%; Score 36; DB 7; Length 2171;
Best Local Similarity 49.5%; Pred. No. 0.11;
Matches 93; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 114 GAATCTCATAGTAAGCGCTGTAGGACTTCGGCTTCTTCAAGCTGTGGAACCATGGTGT 173
DB 180 GAAACAAATGGTTCAGCTGCGAAGAGTGGGGATTTTTTCAANTTGTGAACCATGGAAT 239

QY 174 TCCATTGGAGTTAATGGCCAAATTTAGMAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA 233
DB 240 TCCAAAGACGCTCTTGTAGATGATGCTCTCGAAGAGAAGAACTCTTTGACCAACCTTT 299

QY 234 GTCCGAGAAGACAGAGCTGGTCCCGCCGACCTTTCCGGCTATGTTAGCAAGAGATTGG 293
DB 300 TTCTGTGAAAGTCAGAGAACGTTTTTCGGACTTATCGAAGATAGTTACCGTTGGGAAA 359

QY 294 CCCAAACG 301
DB 360 CCCTAGCG 367

RESULT 7
US-11-174-166-19
; Sequence 19, Application US/11174166
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Kirsch, Wolff M.
; APPLICANT: Lennart, Anton
; APPLICANT: Kelln, Wayne J.
; APPLICANT: Kang, Dae-Kyung
; APPLICANT: Levine, Rodney L.
; APPLICANT: Rouault, Tracey

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; TITLE OF INVENTION: IRON REGULATING PROTEIN-2 (IRP-2) AS
; TITLE OF INVENTION: A DIAGNOSTIC FOR NEURODEGENERATIVE DISEASE
; FILE REFERENCE: LOMAU.140C1
; CURRENT APPLICATION NUMBER: US/11/174,166
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: 60/222,863
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3770
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-11-174-166-19

Query Match      3.5%; Score 35; DB 7; Length 3770;
Best Local Similarity 57.9%; Pred. No. 0.35;
Matches 62; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 783 TAGGGTTTGGCTGACACAAAGTCAAGGTATCAATGATCTACTTTGGAGGACCGC 842
DB 1691 TGGAGTGTTCACCTACCTTAGCAAGCTAGGCTTTGAAATAGTTGGCTATGGATGTTCAAC 1750

QY 843 GTTGAGTCAAAATATAGCACCTTTACCTTCAGTGTGTTAAAGGAG 889
DB 1751 GTGTGTAGGAAATACAGCACCTTTATCAGAAGCAATTTTGAATGCAG 1797

RESULT 8
US-11-117-187-209
; Sequence 209, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 209
; LENGTH: 611587
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-209

Query Match      3.3%; Score 33.2; DB 7; Length 611587;
Best Local Similarity 61.6%; Pred. No. 50;
Matches 53; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 851 AAAATATAGCACCTTTACCTTCAGTGTGTTAAAGGAGAGAGGAGTGTGTTGTTACAAAGACT 910
DB 108621 AAAAAAAAAGCTTCTCTACAGTCAAGATATAAAGAAAGAAATGGTTAAGAAAGACT 108680

QY 911 TCACATGCTGTGAATACAAAGAGGCT 936
DB 108681 TCAAAAGATTATGAATGCAAAAGGCT 108706

RESULT 9
US-11-112-908-140/c
; Sequence 140, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US

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; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-140

Query Match      3.3%; Score 33; DB 7; Length 921;
Best Local Similarity 51.0%; Pred. No. 0.66;
Matches 78; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 381 AGAAATCCTCATCTTTCAGGCGGTGCTGGAGACTACATTACAGCAGTGAAGACAT 440
DB 834 ATATAAGATGACATTTTCAAAATCAGTTGCTGGACAGTAGATTATTCAATAAGGCTGCT 775
QY 441 GTGCTATGCGGTGTTGGAATTGATGCGGAGGGGTTGGGGATAAGCAGCAGGAATACGTT 500
DB 774 GAATTAACCTAGTTAACTAAGGGTAGGAGCCGGGATGGGGATGAGGCTAAGGAGGTGTT 715
QY 501 AAGCAGGTTGCTGAAGGATGAGAAAAGTCAATTC 533
DB 714 GAATAGTTATATCACACACACACCAAAATAAATTC 682

RESULT 10
US-11-112-908-40/c
; Sequence 40, Application US/11/112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
; LENGTH: 180862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-40

Query Match      3.3%; Score 33; DB 7; Length 180862;
Best Local Similarity 51.0%; Pred. No. 26;
Matches 78; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 381 AGAAATCCTCATCTTTCAGGCGGTGCTGGAGAACTACATTACAGCAGTGAAGACAT 440
DB 138122 ATATAAGATGACATTTTCAAAATCAGTTGCTGGACAGTAGATTATTCAATAAAGGCTGCT 138063
QY 441 GTGCTATGCGGTGTTGGAATTGATGCGGAGGGGTTGGGGATAAGCAGCAGGAATACGTT 500
DB 138062 GAAATAACTAGTTAACTAAGGGGTAGGAGCCGGGATGGGGATGAGGCTAAGGAGGTGTT 138003

; CURRENT APPLICATION NUMBER: US/11/117,187
; Sequence 212, Application US/11/117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: FREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 212
; LENGTH: 163317
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-212

Query Match      3.2%; Score 32.2; DB 7; Length 163317;
Best Local Similarity 57.4%; Pred. No. 45;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 768 TAAAGTGTAAGCATAGGTTTTCGCTGACACACGAAGTCAAGTTATCAATGATCTA 827
DB 104835 TAAAAAGGAAAGACTAGTTTTTTTATTACAAACCTCAACACCAATGATCTC 104894
QY 828 CTTTGGAGGACCAGCGGTTTGAGTGAAAAATATAGCACCCTTTAC 868
DB 104895 CAAGTGAGAACCAACCCACACAGAAAAAATTGAAACCTTAC 104935

RESULT 12
US-10-750-185-56890/c
; Sequence 56890, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56890
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-56890

Query Match      3.2%; Score 31.6; DB 6; Length 1138;
Best Local Similarity 47.9%; Pred. No. 2.3;
Matches 91; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 427 GCAGTGAAGAACATGTGCTATCGCGTGTGGAAATTGATGCGGAGGGGTTGGGGATAAG 486
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Db      343  GCTCTCAAGGAATAACCTGTGGGGGAACCTAACTTAAGCAGGAGGAGGGGAAGCAT 284
Qy      487  CAGAGGAATACCTTAAGCAGGTTGCTGAAGGATGAGAAAGTGATTTCGTCTTCAGGTTG 546
Db      283  CTGACATTTAGCTAGGCTGAAGATGAGATGAGCCAGTTATTTAATGTGCTGGGA 224
Qy      547  AACCACTACCCCTTGGCCCTGAGTGCAGCACTGAACCGGAATTTGGTGGGTTGGG 606
Db      223  AAGAATTTCCACGTGAAGAAGTAATGAACCAAGGGCTTGAGTTGAGAGGGCCAGTG 164
Qy      607  GAGCACACAG 616
Db      163  GAGCGGCAG 154

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RESULT 13
US-11-117-187-199
; Sequence 199, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPELHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
; LENGTH: 101786
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-199

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Query Match      3.2%; Score 31.6; DB 7; Length 101786;
Best Local Similarity 55.5%; Pred. No. 53;
Matches 61; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy      142  TTCGGCTTCTTCAAGCTTGTGAACCATGCTGTTCATTTGGAGTTAATGGCCCAATTAGAA 201
Db      46126  TCAACTTCTACAAGCATCTGAGTCGCTTTCTTCATGAGAACTCATCACTAAGTAGAA 46185
Qy      202  AACGAGGCCCTCAGGTTCTTTTAAATAATCTCAGTCCGAGAAAGACAGAGC 251
Db      46186  AACAAATGAACCTCAATTTGATGCACTAACTGCAACAGAGAAATATAAAGGC 46235

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RESULT 14
US-11-121-086-44
; Sequence 44, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 167116
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-44

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Query Match      3.2%; Score 31.4; DB 7; Length 167116;
Best Local Similarity 53.7%; Pred. No. 87;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy      474  GTTGGGATAAGGCAGAGGAATACCTTAAGCAGGTTGCTGAAGGATGAGAAAGTGATTTC 533
Db      30316  CTTGGGATGTTGGTGGCAGTGGTGTGGAGGTGGTAGCAGGAGTGTAGTGGCAGTG 30375
Qy      534  GTGCTTCAGGTTGAACCACTACCCGCTTGGCCCTGAGTGCAGCACTGAACCGGAATTT 593
Db      30376  GTGGTTGGTGTGTGGCAGCAGTGGCGTGTGCTTGTGGCCAGCTATATTCCGGAGGCT 30435
Qy      594  G 594
Db      30436  G 30436

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RESULT 15
US-10-995-561-13474/c
; Sequence 13474, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13474
; LENGTH: 187786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(187786)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-995-561-13474

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```

Query Match      3.2%; Score 31.4; DB 6; Length 187786;
Best Local Similarity 54.9%; Pred. No. 94;
Matches 62; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy      155  AGCTTGTGAACCATGCTGTTCATTTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCA 214
Db      52949  AGTGTGTTACATGCGAGCCCTTCATTTGGTCACCTGAGCATTTTACAAAGGGAACCTGA 52890
Qy      215  GGTTCCTTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCGACCTT 267
Db      52889  GGCTTCTGAAGCAATGACGAGGAGACTGACAGAGGTGGCGAGGCTTGCCTT 52837

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Search completed: December 28, 2005, 01:30:14
Job time : 183.487 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: December 28, 2005, 00:38:54 ; Search time 6072 Seconds
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Title: US-10-670-454-2
Perfect score: 1748
Sequence: 1 MVVLSQPALNQFLFKPKS.....AAYTSRLADNRLAPQKSA 331

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Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
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12: gb.un.*
13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1748	100.0	999	6	CQ899251 Sequence
2	1748	100.0	1318	6	BD243009 Enzyme. 7
3	1748	100.0	1318	6	AR444991 Sequence

4	1748	100.0	1318	6	AX008671 Sequence
5	1748	100.0	1318	15	PC0132438
6	1635	93.5	1360	15	AB181372
7	1530.5	87.6	1359	6	AR528429 Sequence
8	1161	66.4	1245	15	AY594292
9	1132	64.8	1292	15	AB125232
10	1120	64.1	1406	15	AB125232
11	1110	63.5	1479	15	AY588978
12	1105.5	63.2	1383	15	MMY09113
13	1104.5	63.2	1292	15	CMA315663
14	1102.5	63.1	1308	15	AB031206
15	1092.5	62.5	1026	6	CMA302041
16	1092.5	62.5	1026	6	AX506555
17	1092.5	62.5	1026	6	AX506555
18	1092.5	62.5	1026	6	AX506555
19	1092.5	62.5	1026	6	AX506555
20	1092.5	62.5	1026	6	AX506555
21	1092.5	62.5	1026	6	AX506555
22	1092.5	62.5	1026	6	AX506555
23	1092.5	62.5	1026	6	AX506555
24	1069.5	61.2	1306	15	AB125233
25	1068.5	61.1	1352	6	AR452821
26	1067.5	61.1	1229	15	AF506281
27	1060.5	60.7	1365	6	AR452817
28	1060	60.6	1403	6	AR528430
29	1054	60.3	100864	15	AP006391
30	1051.5	60.2	1324	15	AF056935
31	1050	60.1	1281	15	CMA315662
32	1020.5	58.4	1277	15	AF100955
33	1011.5	57.9	983	15	AF101382
34	973	55.7	984	6	AX653573
35	973	55.7	984	15	AB092485
36	973	55.7	1271	15	AK060714
37	973	55.7	1650	6	AR452816
38	973	55.7	1651	15	AK060666
39	973	55.7	1749	15	AK101713
40	972	55.6	1473	6	AR452818
41	972	55.6	1473	15	BT009225
42	970	55.5	1639	15	AK099350
43	965	55.2	1259	15	AB067639
44	963	55.1	1242	15	AB031207
45	957.5	54.8	1555	6	AR452815

ALIGNMENTS

RESULT 1	CQ899251	Sequence 3 from Patent WO2004092390.	999 bp	DNA	linear	PAT 08-NOV-2004
LOCUS	CQ899251	Sequence 3 from Patent WO2004092390.				
DEFINITION	CQ899251					
ACCESSION	CQ899251					
VERSION	CQ899251.1	GI:55583091				
KEYWORDS	Phaseolus coccineus					
SOURCE	Phaseolus coccineus					
ORGANISM	Phaseolus coccineus					
REFERENCE	1	Gilbertson, L., Krieger, E., Zhang, W. and Ye, X.				
AUTHORS		Dna constructs and methods to enhance the production of				
TITLE		commercially viable transgenic plants				
JOURNAL		Patent: WO 2004092390-A 3 28-OCT-2004;				
FEATURES		Monasanto Technology LLC (US)				
	source	1. .999				
		/organism="Phaseolus coccineus"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:3886"				
ORIGIN						

Alignment Scores:


```
Pred. No.: 2,26e-155 Length: 999
Score: 1748.00 Matches: 331
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-670-454-2 (1-331) x Q0899251 (1-999)

Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db 1 ATGGTTGTTCTGCTCAGCAGCATTTGAACCAAGTTTCTTCTGAACCAATTCAGAGTCC 60

Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 61 ACGCCCTTGTTCACGGGGATTCCTGTGTGCGACTCAGCACCCCGATGCCAAGATCTC 120

Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 121 ATAGTGAACGCCCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 180

Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 181 GAGTTAATGGCCAAATTTAGAAAACGAGGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240

Qy 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 241 AAAGACAGAGCTGTCCCCCGACCTTTCGGCTATGTTAGCAGAGGATTTGGCCCAAC 300

Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 301 GGTGATGTGGTGGTTCGAATACCTCCTCAACACCAACCTGATGTTATCTCACCC 360

Qy 121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
Db 361 AAATCACTTTGCAATTTCCGAGAAAATCTCTCATCTTCAAGGCGGTGGTGAGAACTAC 420

Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 421 ATTACAGCAGTGAAGAACATGTCTATGCGTGTGGTGAATGATGCGGGGGTGGGG 480

Qy 161 IleArgLysArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 481 ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTCAAGGATGAGAAAAGTGAATCGTCTTC 540

Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
Db 541 AGGTTGAACCACTACCCGCTTTCGCTGAGGTGCAAGCAGTGAACCGGAATTTGGTGGG 600

Qy 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
Db 601 TTTGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTAACAGCACATCTGCG 660

Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 240
Db 661 TTGCAAAATCTGCTCACAGATGCACTTGGGTTTCACTCCCACTGATCAGACTTCCTTT 720

Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAAGTGAAG 780

Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 781 CATAGGGTTTGGCTGACACACAGAGTCAAGGTTATCAATGATCTACTTTGGAGAGCCA 840

Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
Db 841 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTCAATGTTAAAAAGAGAGAGTGTGG 900

Qy 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 901 TACAAAGAGTTTCATGGTGTGAATACAAAGAGGCTGCGTACACTTCAAGGGCTAGCTGAT 960
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Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCT 993

RESULT 2
BD243009 1318 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Enzyme.
BD243009
ACCESSION
BD243009
VERSION
BD243009.1 GI:33052779
KEYWORDS
JP 2002518005-A/1.
SOURCE
Phaseolus coccineus
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
REFERENCE
1 (bases 1 to 1318)
AUTHORS
Thomas,S.G., Hedden,P. and Phillips,A.L.
JOURNAL
Patent: JP 2002518005-A 1 25-JUN-2002;
THE UNIVERSITY OF BRISTOL
COMMENT
OS Phaseolus coccineus (scarlet runner bean)
PN JP 2002518005-A/1
PD 25-JUN-2002
PF 11-JUN-1999 JP 2000554838
PR 12-JUN-1998 GB 9812821.8,15-JUL-1998 GB 9815404.0 PI
STEPHEN GREGORY THOMAS,PETER HEDDEN,ANDREW LEONARD PHILLIPS PC
C12N9/04,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10, PC
C12N15/09,
PC C12N5/00,C12N5/00,C12N15/00
CC Enzyme
FH Key Location/Qualifiers
FT source 1..1318
FT /organism='Phaseolus coccineus (scarlet runner
bean)',
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Location/Qualifiers
1..1318
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ORIGIN

Alignment Scores:
Pred. No.: 3,17e-155 Length: 1318
Score: 1748.00 Matches: 331
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-670-454-2 (1-331) x BD243009 (1-1318)

Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLysProPheLysSer 20
Db 68 ATGGTTGTTCTGCTCAGCAGCATTTGAACCAAGTTTCTTCTGAACCAATTCAGAGTCC 127

Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 128 ACGCCCTTGTTCACGGGGATTCCTGTGTGCGACTCAGCACCCCGATGCCAAGATCTC 187

Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 188 ATAGTGAACGCCCTGTAGGACTTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 247

Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 248 GAGTTAATGGCCAAATTTAGAAAACGAGGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307

Qy 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 308 AAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAC 367
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Db      1028 AATAGGCTGGCCCTTCCAGAAATCTGCTGCT 1060
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RESULT 4
AX008671
LOCUS      AX008671.1 1318 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9966029.
ACCESSION AX008671
VERSION    AX008671.1 GI:9996195
KEYWORDS   Phaseolus coccineus
SOURCE      Phaseolus coccineus
ORGANISM    Phaseolus coccineus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Phaseolus.
REFERENCE   1
AUTHORS     Phillips,A.L., Hedden,P. and Thomas,S.G.
TITLE        Enzyme
JOURNAL      Patent: WO 9966029-A 1 23-DEC-1999;
            PHILLIPS ANDREW LEONARD (GB); HEDDEN PETER (GB); UNIV BRISTOL (GB);
            THOMAS STEPHEN GREGORY (GB)
FEATURES
source      Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.:      3 17e-155      Length:      1318
Score:          1748.00      Matches:      331
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              6              Gaps:        0

US-10-670-454-2 (1-331) x AX008671 (1-1318)

Qy      1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
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Db      68 ATGGTTGTTCTGCTCAGCCAGCATTTGAACAGATTTTCCTCTGAAACCATTTCAAGTCC 127
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Qy      21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
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Db      128 ACGCCCTTGTTCAGCGGATCTCTGTGTCGACTCAGCCACCCCGATGCCAAGATCTC 187
|||||
Qy      41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
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Db      188 ATAGTGAACGCTGTAGGACTTCGGCTTCTCAAGCTTGTGAACCATGTTCCATTG 247
|||||
Qy      61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
|||||
Db      248 GAGTTAATGGCCAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
|||||
Qy      81 LysAspArgAlaGlyProProAspProPheGlyTyrClySerLysArgIleGlyProAsn 100
|||||
Db      308 AAAGACAGAGCTGTCCCCCGACCCCTTCGGCTATGTGATGAGCAAGAGATTTGCCCAAAC 367
|||||
Qy      101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
|||||
Db      368 GGTGATGTCGGTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCC 427
|||||
Qy      121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
|||||
Db      428 AATACATTTGCATTTTCCAGAAAAATCTCATCATTTACAGGCGGTGGTGGAGAACTAC 487
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Qy      141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
|||||
Db      488 ATTACAGCAGTGAAGAAACATGTGCTATGCCGTGTGGAATGTAGCGGAGGGGTGGGG 547
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Qy      161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
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548 ATAAGGCAGCAGCAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAAGTGATTGCTGCTTC 607
181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
|||||
608 AGGTTGAACCACTACCCGCTTGGCCCTGAGGTGCAAGCACTGAACCGAATTTGGTTGGG 667
|||||
201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
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668 TTTGGGAGCAGACAGACCCACAGATAATTTCTGCTTAAGATCTAAACAGCACATCGGC 727
|||||
221 LeuGlnIleCysLeuThrAspGlyThrTyrValSerValProAspGlnThrSerPhe 240
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728 TTGCAAAATCTGCTCACAGATGCCACTTGGGTTTCAGTCCACCTGATCAGACTTCCCTTT 787
|||||
241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
|||||
788 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAG 847
|||||
261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
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848 CATAGGGTTTGGCTGACACACGAAGTCAAGTTATCAATGATCTACTTTCGAGGACCA 907
|||||
281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
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908 GCGTTGAGTGAAAAATATAGCACCTTTACCTTCAGTGTATGTTAAAGGAGAGGAGTGTGG 967
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301 TyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
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968 TACAAAGAGTTTACATGGTGTGAATCAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
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321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
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1028 AATAGGCTGGCCCTTCCAGAAATCTGCTGCT 1060

RESULT 5
PCO132438      1318 bp mRNA linear PLN 20-APR-1999
LOCUS          Phaseolus coccineus mRNA for GA 2-oxidase, gene ga2ox1.
DEFINITION     AJ132438
ACCESSION      AJ132438
VERSION        AJ132438.1 GI:4678585
KEYWORDS       GA 2-oxidase; ga2ox1 gene.
SOURCE         Phaseolus coccineus
ORGANISM       Phaseolus coccineus
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
               Phaseolus.
REFERENCE       1
AUTHORS        Thomas,S.G., Phillips,A.L. and Hedden,P.
TITLE          Molecular cloning and functional expression of gibberellin 2-
               oxidases, multifunctional enzymes involved in gibberellin
               deactivation
JOURNAL         Proc. Natl. Acad. Sci. U.S.A. 96 (8), 4698-4703 (1999)
PUBMED         10200325
REFERENCE       2 (bases 1 to 1318)
AUTHORS        Phillips,A.L.
TITLE          Direct Submission
JOURNAL         Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long
               Ashton Research Station, Long Ashton Research Station, Bristol,
               BS41 9AP, UK
FEATURES
source         Location/Qualifiers
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 IQRNTLRLLKXEDSCFRLNHYPPCPVEQALNRNLVGFGEHTDPOIISVLRNST
 SGLQICLDGTGTVSPVPPQTSFFINVGDALQVMTNGRFRKSVKRVLRVADITKSRLSMIY
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ORIGIN

Alignment Scores:
 Pred. No.: 3.17e-155 Length: 1318
 Score: 1748.00 Matches: 331
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-10-670-454-2 (1-331) x PCO132438 (1-1318)

QY	1	MetValValLeuSerGlnProAlaLeuEngInPhePheLeuLeuLysProPheLysSer	20
DB	68	ATGGTGTGTTCTCTCAGCCAGCATGAACCAAGTTCCTCTCTGAAACCATTCAGTCC	127
QY	21	ThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysAsnLeu	40
DB	128	AGCCCTTGTTACGGGAGTCTCTGTGTCAGCTCAGCACCCCGATGCCAAGATCTC	187
QY	41	IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu	60
DB	198	ATAGTGAACCGCTGTAGGACTTCGGCTCTTCAAGCTTGTAACCATGTTCCATTG	247
QY	61	GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu	80
DB	248	GAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	307
QY	81	LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn	100
DB	308	AAAGACAGAGCTGGTCCCGCCAGCCCTTTCGGCTATGTAGCAAGAGATGGCCCAAC	367
QY	101	GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValLysSerPro	120
DB	368	GGTGATGTCGGTGGTGCAGTACCTCTCTCTCAACCAACCTGATGTTATCTCACCC	427
QY	121	LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValAlaGluAsnTyr	140
DB	428	AAATCACTTTCATTTTCCGAGAAATCTCATCTATTTTCAGGCGGTGGTGAGAACTAC	487
QY	141	IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly	160
DB	488	ATTACAGCAGTGAAGAACATGTCTATCGGTGTTGGAAATGATGCGGAGGGTGGGG	547
QY	161	IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe	180
DB	548	ATAAGCGCAGAGGATAGCTTAAGCAGGTTCCTGTAAGGATGAGAAAAGTGATTCGTCTTC	607
QY	181	ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly	200
DB	608	AGGTTGAACCACTACCCCGCTTCGCGCTGAGGTGCAAGCACTGAACCGGAAATTTGGTGGG	667
QY	201	PheGlyGluHisThrAspProGlnIleLysSerValLeuAspSerAsnSerThrSerGly	220
DB	668	TTTGGGGAGCACACAGACCACAGATAATTTCTGCTTAAAGATCTAACAGCACATCTGCG	727
QY	221	LeuGlnIleCysLeuThrAspGlyThrTyrValSerValProProAspGlnThrSerPhe	240
DB	728	TTGCAAACTGCTCACAGATGGCCTGGTTCCTGATCCCACTGATCAGACTTCCTTT	787
QY	241	PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys	260
DB	788	TTTCATCAATGTTGGTGCAGCTCTACAGGTAATGACTAATAGGGAGGTTTAAAAAGTGAAG	847

QY	261	HisArgValLeuAlaAspThrThryLysSerArgLeuSerMetIleTyrPheGlyGlyPro	280
DB	848	CATAGGGTTTTGGCTGCACACAAGTCAAGGTATCAATGATCTACTTTGGAGGACCA	907
QY	281	AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlnCysLeu	300
DB	908	CGCTTGAGTGAATAATATAGCACCTTTACCTTCAGTGATGTTAAAGAGGAGAGGTGTTTG	967
QY	301	TyrLysGluPheThrTyrCysGluTyrLysLysAlaIleTyrThrSerArgLeuAlaAsp	320
DB	968	TACAAAGAGTTCACATGGTGTGAATACAAAGAGGCTGGTACACTTCAAGGCTAGCTGAT	1027
QY	321	AsnArgLeuAlaProPheGlnLysSerAlaAla	331
DB	1028	AATAGGCTGGCCCTTTCAGAAATCTGCTGCT	1060

RESULT 6

AB181372

LOCUS

DEFINITION

cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

JOURNAL

FEATURES

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1. 1360

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83. 1081

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IQRNTLRLLKXEDSCFRLNHYPPCPVEQALNRNLVGFGEHTDPOIISVLRNST

SGLQICLDGTGTVSPVPPQTSFFINVGDALQVMTNGRFRKSVKRVLRVADITKSRLSMIY

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ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

1.53e-144

1635.00

96.36%

Length:

Matches:

Conservative:

1360

311

7

Best Local Similarity: 94.24%		Mismatches: 12	
Query Match: 93.54%		Indels: 0	
DB: 15		Gaps: 0	
US-10-670-454-2 (1-331) x AB181372 (1-1360)			
QY	1	MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer	20
DB	83	ATGGTTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTTTCGTTCTGAAACCAATCGAAGTCC	142
QY	21	ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu	40
DB	143	AGCCCTTTGTCACGGGATTCCTGTGTGTCGATTCACGCACCCCGATGCCAAGAACTC	202
QY	41	IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu	60
DB	203	ATAGTGGAGCCCTGTAGGACTACGGCTTCTTCAAGCTCGTGAACCATGTGTTCATTG	262
QY	61	GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu	80
DB	263	GAGTTAGTGGCCAAATTTAGAAACGAAGCCCTCAGGTTCTTCAAAAATCTCAGTCAGAG	322
QY	81	LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn	100
DB	323	AAAGACAGGGCTGGTCCCGCCGACCTTTCGGCTACGGTAGCAAGGGGATTTGGCCCAAC	382
QY	101	GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro	120
DB	383	GCGGATGTGGTGGTTCGAACTCTCTCCCAACCAACCCCTGAGGTCAATCTCACCC	442
QY	121	LysSerLeuCysIlePheArgGluAenProHisHisPheArgAlaValValGluAenTyr	140
DB	443	AAATCACTCTCCATTTTCGCTGAAGTCTCATCTTCAGGGCGGTGTGGAGAACTAC	502
QY	141	IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly	160
DB	503	ATTACAGCAGTAAAGAACATGTGTATGCGGTGTGGAAATTTGATGGCAGAGGGTTCGGG	562
QY	161	IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe	180
DB	563	ATAGCCAGAGGAATACCTTAAGCAGGTGCTGGAAGGATGAAAGTAGTCAATGCTTC	622
QY	181	ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly	200
DB	623	AGGATGAACCACTACCCGCGTGCACAGAGGTGCCAGACTGAACCGGAATTTGGTTGGG	682
QY	201	PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly	220
DB	683	TTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAATAGCACATCAGGC	742
QY	221	LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe	240
DB	743	TTGCAAACTGTCTCGAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTT	802
QY	241	PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys	260
DB	803	TTTCATCAATGTTGGTGATGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAG	862
QY	261	HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro	280
DB	863	CATAGGGTTTGGCTGACACACGAAGTCAAGGTTATCAATGATATACATTTTGGAGGACCA	922
QY	281	AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysLeu	300
DB	923	GGCTCAGTGAAAGATAGCACTTTACCTTTCAGTGTGTAAGAGGAGGAAAGTTTG	982
QY	301	TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp	320
DB	983	TACAAAGAGTTACATGGTGGGAATACAGAAGGCTGGGTACACTTCAAGGCTAGCTGAT	1042
QY	321	AsnArgLeuAlaProPheGlnLysSerAla	330
DB	1043	AATAGGCTTGGCCCTTTTCGAGAAATCTGCT	1072

RESULT 7		1359 bp DNA linear		PAT 08-OCT-2004	
AR528429		Sequence 62 from patent US 6723897.			
DEFINITION		AR528429			
ACCESSION		AR528429.1		GI:53916494	
VERSION		AR528429.1			
KEYWORDS		Unknown.			
SOURCE		Unknown.			
ORGANISM		Unclassified.			
REFERENCE		1 (bases 1 to 1359)			
AUTHORS		Brown, S.M., Elich, T.D., Heck, G.R., Kishore, G.M., Logusch, E.W., Logusch, S.J., Piller, K.J., Rao, S., Ream, J.E. and Baerson, S.R.			
TITLE		Methods for controlling gibberellin levels			
JOURNAL		Patent: US 6723897-A 62 20-APR-2004;			
FEATURES		Monsanto Technology, LLC; St. Louis, MO			
source		1..1359			
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ORIGIN					
Alignment Scores:					
Pred. No.:		1.12e-134		Length: 1359	
Score:		1530.50		Matches: 296	
Percent Similarity:		90.36%		Conservative: 4	
Best Local Similarity:		89.16%		Mismatches: 31	
Query Match:		87.56%		Indels: 1	
DB:		6		Gaps: 1	
US-10-670-454-2 (1-331) x AR528429 (1-1359)					
QY	1	MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer	20		
DB	102	ATGGTTGTTCTGTCTCAGCCAGCATTTAAACCAAGTTTTCCTTCTGAAACACATGCAAGCCC	161		
QY	21	ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu	40		
DB	162	ACGCCCTTGTTCGCGGGATTCCTGTGTGTCGACTCGAGCCCGCATGCCAAGACCCAC	221		
QY	41	IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu	60		
DB	222	ATAGTCAATGCTCGAGGACTTCGGCTTCTTCAAGCTCGTGAACCCACCGTGTTCGGTTA	281		
QY	61	GluLeuMetAlaAsnLeuGluAenGluAlaLeuArgPhePheLysLysSerGlnSerGlu	80		
DB	282	CAGTTTCATGGCCCAATTTGGAAACGAAACCCCTCGGGTCTTCAAAAAACCTCAATCCGAG	341		
QY	81	LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn	100		
DB	342	AAAGACAGGGCTGGTCCCTCGACCTTTTGGCTAGCGCAGCAAGAGGATTTGGCCCTAAC	401		
QY	101	GlyAspValGlyTrpValGluTyrLeuLeuLeuAenThrAsnProAspValIleSerPro	120		
DB	402	GGCGATGTGGTGGTTCGAAATACCTCTCTCAACCAACCCCTGATGTCATCTCCCC	461		
QY	121	LysSerLeuCysIlePheArgGluAenProHisHisPheArgAlaValValGluAenTyr	140		
DB	462	AAAGTCAAGTTCATTTTCAGAGAAGTCTCTCAGAAATTTTCAGGGCGGTGTGGAGGAATAC	521		
QY	141	IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly	160		
DB	522	ATTAGACCGGTGAGAACATGTGCTATGAGGTGTGGAAATGATGCTCAGGGATTGGGG	581		
QY	161	IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe	180		
DB	582	ATAACGACAGGAATGTGTGATAGTGTGCTGAGGATGAGAGAGTGTATCTTCCTTC	641		
QY	181	ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAen--ArgAsnLeuVal	199		
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QY 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
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QY 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097

RESULT 8
AY594292 1245 bp mRNA linear PLN 30-APR-2005
LOCUS Neriium oleander GA 2-oxidase 2 mRNA, complete cds.
DEFINITION AY594292
ACCESSION AY594292.1 GI:51011365
VERSION
KEYWORDS
SOURCE Neriium oleander (common oleander)
ORGANISM Neriium oleander
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
asterids; lamiales; Gentianales; Apocynaceae; Apocynaceae;
Wrightiaceae; Neriium.
REFERENCE 1 (bases 1 to 1245)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Isolation, characterization and multi-site polyadenylation of GA
20-oxidases and GA 2-oxidases in Neriium oleander
Unpublished
JOURNAL 2 (bases 1 to 1245)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Direct Submission
Submitted (08-APR-2004) Instituto de Biologia Molecular y Celular
de Plantas, Consejo Superior de Investigaciones Cientificas (CSIC),
Universidad Politecnica de Valencia, Avda. de los Naranjos s/n,
Valencia 46022, Spain
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CDS
ORIGIN
Alignment Scores:

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Pred. No.: 7.65e-100 Length: 1245
Score: 1161.00 Matches: 216
Percent Similarity: 82.23% Conservative: 57
Best Local Similarity: 65.06% Mismatches: 57
Query Match: 66.42% Indels: 2
DB: 15 Gaps: 2
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QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
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QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 121 CTGTGTAAGGCTGTCAAGAGTTTGGATTTTCAAGATCATTAATCAGCGTGTTCACACC 180
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Db 958 GATAACAGACTGGTCTGTTGAGAAAATTGCTGCC 993

RESULT 9
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LOCUS Nicotiana tabacum GA20x1 mRNA for gibberellin 2-oxidase 1, complete cds.
DEFINITION
AB125232
VERSION
SOURCE
KEYWORDS
ORGANISM Nicotiana tabacum (common tobacco)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1
REFERENCE
AUTHORS Sakane, M., Nakajima, M. and Yamaguchi, I.
JOURNAL Molecular cloning of GA 2-oxidase in BY-2
TITLE Unpublished
2 (bases 1 to 1292)
AUTHORS Sakane, M., Nakajima, M. and Yamaguchi, I.
JOURNAL Direct Submission
TITLE Submitted (28-OCT-2003) Masayuki Sakane, University of Tokyo,
Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo
113-0032, Japan (E-mail: m-sakane@gr1.ch.a.u-tokyo.ac.jp,
URL: http://pgr1.ch.a.u-tokyo.ac.jp/, Tel: 81-3-5841-5158 (ex. 25158),
Fax: 81-3-5841-8025)
FEATURES
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Best Local Similarity: 64.16% Mismatches: 68
Query Match: 64.76% Indels: 2
DB: 15 Gaps: 2

US-10-670-454-2 (1-331) x AB125232 (1-1292)

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Qy 21 ThrProLeuPheThrGlyIleProValAlaPheLeuThrHisProAspAlaLysAsnLeu 40
Db 135 TCCTCATCTTCAATGGTGTTCATTCATAGACCTCTCTAAACCTAACTAAGAACCTT 194

Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 195 ATGTGTAAGCCCTGTGAAGAATTGGATTCTTCAAAGTCATTAACCATAGCGTCCCTACG 254

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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1406)
AUTHORS Ubada-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
TITLE Direct Submission
JOURNAL Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas,
CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn,
Valencia 46022, Spain
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ACCESSION Y09113
VERSION Y09113.1 GI:1666095
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SOURCE Marah macrocarpus
ORGANISM Marah macrocarpus
REFERENCE 1 MacMillan,J., Ward,D.A., Phillips,A.L., Sanchez-Beltran,M.J.,
AUTHORS Gaskin,P., Lange,T. and Hedden,P.
TITLE Gibberellin biosynthesis from gibberellin A12-aldehyde in endosperm
and embryos of Marah macrocarpus
JOURNAL Plant Physiol. 113 (4), 1369-1377 (1997)
PUBMED 9112781
REFERENCE 2 (bases 1 to 1479)
AUTHORS Hedden,P.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1996) P. Hedden, University of Bristol,
Department of Agricultural Sciences, IACR-Long Ashton Research
Station, Long Ashton, Bristol, BS18 9AP, UK
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QY	141	IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly	160						
DB	556	ATCTGGGCTGTGAGAACATGGCGTGTGAATCGTAGATTAAATGGCGAAGGTTGAAG	615						
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QY	199	ValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThr	218						
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DB	796	TCGTGACTTCAAAATTTCTCTCCCTGATGCCAATTTGGATTCTGTTCCTCTGATCAAACT	855						
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DB	856	TCCTTCTTCATCAATGTTGGTGACTCTTTACAGGTGATGACTAATGGAAGGTTCAAAAGT	915						
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Db	544	TTACAGAGTGAACCATTAATCCGCGCATGTCCAGACCTTCAAGCTTTAAAGGAACAAACATG	603
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Qy	239	SerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSer	258
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Qy	259	ValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGly	278
Db	784	GTGAAGCATAGGGTTTTGACAAACAGCTCGAAGTCAGGGTTCAATGATCTACTTCCGT	843
Qy	279	GlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlu	298
Db	844	GGGCCACCGTTGAGTGAAGAAATAGCTCTCTTTAGCTTCCCTTATCAAGGAGAAAGAA	903
Qy	299	CysLeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaIleTyrThrSerArgLeu	318
Db	904	AGTTTGTACAAAGAGTTTACATGGTTTTCAGTACAAAGATCAGCTTACAACCTCCAGTTG	963
Qy	319	AlaAspAsnArgLeuAlaProPheGlnLysSerAlaAla	331
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RESULT 13			
ABO31206			
LOCUS			
DEFINITION			
ABO31206			
ACCSSION			
VERSION			
KEYWORDS			

RESULT 13
AB031206
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

SOURCE	Lactuca sativa
ORGANISM	Lactuca sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
REFERENCE	1 Nakaminami,K., Sawada,Y., Suzuki,M., Kenmoku,H., Kawaide,H., Mitsuhashi,W., Sassa,T., Inoue,Y., Kamiya,Y. and Toyomasu,T. Deactivation of gibberellin by 2-oxidation during germination of photoblastic lettuce seeds Biosci. Biotechnol. Biochem. 67 (7), 1551-1558 (2003)
AUTHORS	Toyomasu,T., Mitsuhashi,W. and Kamiya,Y.
TITLE	Direct Submission Submitted (17-AUG-1999) Tomonobu Toyomasu, Yamagata University, Faculty of Agriculture; Wakaba-cho 1-23, Tsuruoka, Yamagata 997-8555, Japan (E-mail:toyomasa@tdel.tr.yamagata-u.ac.jp, Tel:81-235-28-2861, Fax:81-235-28-2812)
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Alignment Scores:	
Pred. No.:	1.73e-94 Length: 1292
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Percent Similarity:	78.34% Conservative: 51
Best Local Similarity:	63.20% Mismatches: 66
Query Match:	63.19% Indels: 7
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Db	929	ATCTATTTTGGAGGACCACCAATTGAGCGAGAAGTAGCACCATTGCCATCACTTATACAA	988
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DEFINITION	Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene).		
ACCESSION	AJ302041		
VERSION	AJ302041.1	GI:27123664	
KEYWORDS	ga2ox gene; gibberellin 2-oxidase.		
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ORGANISM	Cucurbita maxima		
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REFERENCE	1		
AUTHORS	Frise, A. and Lange, T.		
TITLE	Expression studies on the major Gibberellin dioxygenases in developing seeds of Cucurbita maxima L		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1308)		
AUTHORS	Lange, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-DEC-2000) Lange T., Botanical Institute, Dept. Plant Physiology and Biochemistry, TU Braunschweig, Mendelssohnstr. 4, Braunschweig, D-38106, GERMANY		
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DEFINITION Sequence 1350 from Patent WO0216655.
ACCESSION AX506655
VERSION AX506655.1 GI:23387892
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
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REFERENCE Harper,J.F., Krens,J., Wang,X. and Zhu,T.
AUTHORS Stress-regulated genes of plants, transgenic plants containing
TITLE same, and methods of use
JOURNAL Patent: WO 0216655-A 1350 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations AG
(CH)
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Job time : 6080 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Maximum Match 100%

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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ID ADT62692 standard; DNA; 999 BP.
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AC ADT62692;
XX
DT 13-JAN-2005 (first entry)
DE DNA encoding Phaseolus coccineus gibberellin 2-oxidase.

XX DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene;
XX expression cassette; transgenic plant; transgenic; plant;
XX gibberellin 2-oxidase; ds.
XX Phaseolus coccineus.
XX WO2004092390-A2.
XX 28-OCT-2004.
XX 09-APR-2004; 2004WO-US011000.
XX 09-APR-2003; 2003US-0461459P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Gilbertson L, Krieger E, Zhang W, Ye X;

DR WPI; 2004-758349/74.
 XX New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
 PT first border region linked to a transgene linked to an Agrobacterium Ti
 PT plasmid second border region, useful for enhancing production of
 PT transgenic plants.
 XX

Example 1; SEQ ID NO 3; 77pp; English.

XX The present invention relates to a DNA plasmid comprising a transfer DNA
 CC (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
 CC to at least one transgene linked to an Agrobacterium Ti plasmid second
 CC border region, and located in the DNA plasmid outside of the T-DNA is a
 CC plant expression cassette comprising a plant cell non-lethal negative
 CC selectable marker gene linked to a vector backbone DNA. Also disclosed
 CC are a method for enhancing the selection of transgenic plants that do not
 CC contain vector backbone DNA, a method for reducing the copy number of a
 CC transgene in a plant cell, and a transgenic plant produced by the method.
 CC The DNA plasmid comprises the expression cassette comprising a promoter
 CC that functions in plant cells operably linked to a plant cell non-lethal
 CC negative selection marker gene. The promoter is a constitutive promoter.
 CC The promoter expresses the linked non-lethal negative selection marker.
 CC Gene product in tissue culture during plant regeneration. The plant cell
 CC non-lethal negative selectable marker gene comprises a plant hormone
 CC biosynthetic pathway gene, degradative gene, biosynthetic pathway
 CC substrate-diverting gene or signalling gene, or metabolic interference
 CC gene. The transgene is a plant positive selectable marker gene selected
 CC from antibiotic resistance and herbicide resistance. The transgene
 CC comprises a transgene of agronomic interest. The plant hormone
 CC biosynthetic pathway gene is selected from gibberellic acid pathway
 CC genes, cytokinin pathway genes, auxin pathway genes, ethylene pathway
 CC genes, and abscisic acid pathway genes. The plasmid is useful for
 CC enhancing the production of commercially viable transgenic plants. The
 CC present sequence represents DNA encoding Phaseolus coccineus gibberellin
 CC 2-oxidase. The sequence is used as a non-lethal negative selectable
 CC marker gene.

SQ Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,61e-180 Length: 999
 Score: 1748.00 Matches: 331
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-670-454-2 (1-331) x ADT62692 (1-999)

QY 1 MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer 20
 Db 1 ATGGTTGTTCTGTCTCAGCAGCATTGAACCAAGTTTCTTCTGAAACCATTCAGTCC 60
 QY 21 ThrProLeuPheThrGlyIleProValValAspPheGlyPhePheLeuValAsnHisGlyValProLeu 40
 Db 61 ACGCCCTTGTTCACGGGATTCCTGTGTGCGACCTCAGCCACCCGATGCCAAGATCTC 120
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValValAsnHisGlyValProLeu 60
 Db 121 ATAGTGAACCGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTCATTG 180
 QY 61 GluLeuMetAlaAsnLeuGluAenGluAlaLeuAtpPhePheLysLysSerGlnSerGlu 80
 Db 181 GAGTTAATGGCCAAATTTAGAAACGAGGCCCTCAGGTCTTTTAAATAATCTCAGTCCGAG 240
 QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrglyserLysArgIleGlyProAsn 100
 Db 241 AAAGACAGAGCTGGTCCCCCGACCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAC 300
 QY 101 GlyAspValGlyTrrpValGluTyrLeuLeuLeuAenThrAsnProAspValIleSerPro 120
 Db 301 GGTGTATGTCGGTTGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCC 360

QY 121 LysSerLeuCysIlePheArgGluAenProHisHisPheArgAlaValValGluAenTyr 140
 Db 361 AAATCACTTTGGCATTTTCGAGAAATCTCATCATTTTCAGGGCGGTGGTGAGAACTAC 420
 QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuLeuGluLeuMetAlaGluGlyLeuGly 160
 Db 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAAATTGATGCGGAGGGTTGGGG 480
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 Db 481 ATAAAGCAGAGAAATACGTTTAAGCAGGTTCGTGAAGAGATGAGAAAGTGAATTCGTGCTTC 540
 QY 181 ArgLeuAenHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
 Db 541 AGTTTGAACCACTACCCCGCTTCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGG 600
 QY 201 PheGlyGluHisThrAspProGlnIleleSerValLeuArgSerAsnSerThrSerGly 220
 Db 601 TTTGGGAGCAGCACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGGC 660
 QY 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 240
 Db 661 TTGCAAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTT 720
 QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyVargPheLysSerValLys 260
 Db 721 TTCATCAATGTTGGTGAAGCTCTACAGGTAAATGACTAATGGAGGTTTAAAGTGTAAAG 780
 QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
 Db 781 CATAGGGTTTGGCTGACACACCAAGGTCAAGGTATCAATGATCTACTTTTGGAGGACCA 840
 QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
 Db 841 GCGTTGAGTGAATAATATAGCACTTTTACCTTCAGTGATGTTAAAGAGGAGAGGAGTGTG 900
 QY 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
 Db 901 TACAAAGAGTTTCACATGGTGTGAATACAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
 QY 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
 Db 961 AATAGGCTTGGCCCTTTCAGAGAAATCTGCTGCT 993
 RESULT 2
 AAZ55912
 ID AAZ55912 standard; cDNA; 1318 BP.
 XX
 AC AAZ55912;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Runner bean gibberellin 2-oxidase PCGA2ox1 cDNA.
 XX
 KW Gibberellin 2-oxidase; PCGA2ox1; runner bean; 2-beta-hydroxylation;
 KM inactivation; growth inhibition; ss.
 XX
 OS Phaseolus coccineus.
 XX
 FH Key Location/Qualifiers
 FT CDS 68..1066
 FT /*tag= a
 FT /product= "Gibberellin 2-oxidase PCGA2ox1"
 FT /transl_except= (pos:1058..1063, aa:Ala)
 XX
 PN WO9966029-A2.
 PD 23-DEC-1999.
 XX
 PF 11-JUN-1999; 99WO-GB001857.
 XX
 PR 12-JUN-1998; 98GB-00012821.
 PR 15-JUL-1998; 98GB-00015404.

PN W0200009722-A2.
 XX 24-FEB-2000.
 XX 10-AUG-1999; 99WO-US018066.
 XX 10-AUG-1998; 98US-0096111P.
 PR 07-JUN-1999; 99US-013797P.
 XX (MONS) MONSANTO CO.
 XX Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Piller KJ, Rao S, Ream JE;
 XX P-PSDB; AAY84039.
 DR WPI: 2000-224351/19.
 XX P-PSDB; AAY84039.
 XX Obtaining transgenic plant useful for controlling seed germination and
 PT seedling growth comprises transgene comprising a sequence expressing
 PT altered levels of an essential hormone.
 XX Claim 45; Page 248; 267pp; English.
 XX The present sequence encodes a gibberellic acid 2-oxidase 1 protein
 CC sequence, which is used in the method of the invention. The specification
 CC describes methods for the inhibition and control of gibberellic acid
 CC levels. Gibberellic acid levels may be inhibited or controlled by use of
 CC a chimeric expression construct expressing a RNA or protein which
 CC suppresses the gibberellin biosynthetic pathway sequence, diverts
 CC substrate from the pathway, or degrades pathway substrates or products.
 CC The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-
 CC oxidase, phytoene synthase, C-20 oxidase, and a 2beta.3beta-hydroxylase
 CC polynucleotides to achieve this. The method is used to control seed
 CC germination and seedling growth especially to regulate gene products of
 CC gibberellin biosynthetic pathway and restoration of normal seed
 CC germination, in transgenic plants. The plants produced are gibberellin
 CC deficient, and have shortened hypocotyl and/or epicotyl phenotypes
 CC compared to normal plants
 XX SQ Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 2,05e-156 Length: 1359
 Score: 1530.50 Matches: 296
 Percent Similarity: 90.36% Conservative: 4
 Best Local Similarity: 89.16% Mismatches: 31
 Query Match: 87.56% Indels: 1
 DB: 3 Gaps: 1

US-10-670-454-2 (1-331) x AA299471 (1-1359)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
 Db 102 ATGGTTGTTCTGCTCAGCAGCATTAACACAGTTTTTCTCTGAAACATGCAAGCC 161
 QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 Db 162 ACGCCCTTGTTCGGGGATTCTGTGGTGCGACTTCTCAAGTCTCGGACCCCGATGCCAAGACCCAC 221
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 Db 222 ATAGTCAATGCTCGAGGACTTCGGCTTCTTCAAGTCTGTAACACCGTGTTCGGTGA 281
 QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuAArgPhePheLysLysSerGlnSerGlu 80
 Db 282 CAGTTTCATGCGCAATTTGGAAACGAAACCCCTCGGGTTCTTCAAAAAACCTCAATCCGAG 341
 QY 81 LysAsnArgAlaGlyProProAspProPheGlyThrGlySerLysArgIleGlyProAsn 100
 Db 342 AAAGACAGGGCTGGTCCCCCTGACCCCTTTGGGTACGGCAGCAAGAGGATGGCCCTAAC 401
 QY 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120

Db 402 GCGCATGTCGGTTGGGTGGAATACCTCTTCTCAACACCAACCTGATGTCATCTCCCC 461
 QY 121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
 Db 462 AAGTCACAGTTTCATTTTCAGAGAAGGTCTCTCAGAAATTCAGGGCGGTGTGGAGNATAC 521
 QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
 Db 522 ATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTGGAAATTCATGCTGAGGGATTGGGG 581
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSerAspSerCysPhe 180
 Db 582 ATAACGACAGGAATGTGTGTAGTAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
 QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn--ArgAsnLeuVal 199
 Db 642 AGACTTTAACCACTACCCGCCATGCCCGAGGTGCAAGCAATTGAACGAAGGAATTTGGTT 701
 QY 200 GlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSer 219
 Db 702 GGATTTGGAGAGCACACAGACCCACAGATAATTTCTGCTCTGAGATCTAACAGCACCTCA 761
 QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSer 239
 Db 762 GGCCTGCAAAATCTGTCTACAGATGGCACTTGGGTTTCTGTCCACCTGATCAAACTTCC 821
 QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
 Db 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTTAATGGGAGGTTTAAAGTGTA 881
 QY 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
 Db 882 AAGCATAGAGTTTGGCTGACCCCAACCAAGTCAAGTTGTCAATGATCTACTTTGGAGCA 941
 QY 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
 Db 942 CCACCCCTTGTGTGAAAAGATAGCACCTTTACCTTCACTCATGTATAAAGAGAGAGAGT 1001
 QY 300 LeuTyrLysGluPheThrTrpCysGluTyrLysAlaAlaTyrThrSerArgLeuAla 319
 Db 1002 TTCTCAAAAGAGTTCACATGGTGGGAATACAAGAGCTGCGTACCGTCAAGGCTAGCG 1061
 QY 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
 Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097
 RESULT 4
 AAD40261
 ID AAD40261 standard; cDNA; 1359 BP.
 XX AAD40261;
 AC AAD40261;
 XX 22-OCT-2002 (first entry)
 DT 22-OCT-2002 (first entry)
 XX Soybean GA 2-oxidase 1 cDNA.
 DE Gibberellin; transgenic plant; seed germination; seedling growth;
 KW transgenic; 2-oxidase 1; enzyme; GA; soybean; gene; ss.
 XX Glycine max.
 OS Glycine max.
 XX Key Location/Qualifiers
 FH 102..1103
 FT /tag= a
 FT /product= "GA 2-oxidase 1 protein"
 FT /transl_except= (pos:633..635, aa:Xaa)
 FT /note= "Xaa = any amino acid"
 XX US2002053095-A1.
 PN 02-MAY-2002.
 XX 10-AUG-1999; 99US-00371307.
 PF

XX 10-AUG-1999; 99US-00371307.
 XX (BROW/) BROWN S M.
 XX Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 XX Pillier KJ, Rao S, Ream JE;
 XX WPI; 2002-489107/52.
 DR P-PSDB; AAE24921.
 XX
 XX Control of gibberellin levels in plants useful to avoid unfavorable
 PT conditions in crops to increase yields, using transgenic plants having
 PT reduced seed germination and early seedling growth then treatment to
 PT restore these properties.
 XX
 XX Claim 45; Page 92-93; 155pp; English.
 XX
 XX The invention relates to control of gibberellin (GA) levels in plants.
 CC The method involves producing transgenic plants having a phenotype of
 CC reduced seed germination and reduced early seedling growth, then
 CC restoring seed germination and early seedling growth by treating plants
 CC with an appropriate compound when conditions are favourable. The method
 CC is useful to control seed germination and/or early seedling growth in
 CC agricultural production so that unfavorable environmental conditions
 CC normally reducing agronomic output can be avoided and yields increased.
 CC Plants also demonstrate increased uniformity of germination, emergence
 CC and seedling vigor, so increasing yields at harvest. The method is
 CC especially useful in crop plants such as e.g. canola, soybean, cotton,
 CC etc., and is also useful in storage and transport of seeds to reduce
 CC premature germination which may affect agronomic or food quality of the
 CC seeds. The present sequence is soybean GA 2-oxidase 1 cDNA
 XX
 XX Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
 SQ

Alignment Scores:
 Pred. No.: 2,05e-156 Length: 1359
 Score: 1530.50 Matches: 296
 Percent Similarity: 90.36% Conservative: 4
 Best Local Similarity: 89.16% Mismatches: 31
 Query Match: 87.56% Indels: 1
 DB: 6 Gaps: 1

US-10-670-454-2 (1-331) x AAD40261 (1-1359)

QY 1 MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLeuYsProPheLeuSer 20
 DB 102 ATGGTTGTTCTGTCTCAGCCGACATTAACCAAGTTTCTCTTCTGAAACATGCAAGCCC 161
 QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLeuAsnLeu 40
 DB 162 AGCCCTTGTTTGGGGGATTCCTGTGCTGACCTCAGGACCCGATGCCAGACCCAC 221
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
 DB 222 ATAGTCAATGCTCGAGGACCTCGGCTTCTTCAAGCTCGTGAACCAACGCTGTCGTTA 281
 QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLeuYsSerGlnSerGlu 80
 DB 282 CAGTTTCATGGCCAAATTTGGAACCAACCCCTCGGGTCTTCAAAACCACTCAATCCGAG 341
 QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrrGlySerLysArgIleGlyProAsn 100
 DB 342 AAAGACAGGCTGTGTCCTCCCTGACCTTTGGCTACGCGAGCAAGAGGATTCGCCCTAAC 401
 QY 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
 DB 402 GCGATGTCGTTGGTTCGATACCTCTTCAACCAACCACTGATGTCATCTCCCC 461
 QY 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
 DB 462 AAGTCACAGTTCATTTTCAGAGAAGGTCCTCAGAATTTTCAGGCGGTGGTGGAGGAATAC 521

QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGlyLeuGly 160
 DB 522 ATTAGAGCGGTGAAGAACATGTCTATGAGGTGTGGAAATGATGGCTGAGGATTTGGG 581
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 DB 582 ATACGCGAGAGGAATGTGTTCAGTAGGTTCGTGAAGGATGAGAAGAGTGATCTTGTCTTC 641
 QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn---ArgAsnLeuVal 199
 DB 642 AGACTTAACCACTACCGCCCATGCCGAGGTGCAAGCATTTGAACGGAAGGAATTTGGTT 701
 QY 200 GlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSer 219
 DB 702 GGATTTGGAGAGCACACAGACCCACAGATAATTTCTGTCTTGAGATCTAACAGCACCTCA 761
 QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProProAspGlnThrSer 239
 DB 762 GGCCTGCAAAATCTGTCTCAGATGGCACTTGGGTTTCTGTCACCTGATCAAACTTCC 821
 QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
 DB 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTATATGACTAATGGGAGGTTTAAAGTGTA 881
 QY 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
 DB 882 AAGCATAGAGTTTGGCTGACCCCAACCAAGTCAAGTTGTCAATGATCTACTTTGGAGGA 941
 QY 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
 DB 942 CCACCTTGTGTGAAGATAGCACCTTTTACCTTCATCTGTTAAAGGAGGAAGAGT 1001
 QY 300 LeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAla 319
 DB 1002 TTCACAAAGAGTTCACATGGTGGGAATACAAGAGGCTCGCTACGCTCAAGGCTAGCG 1061
 QY 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
 DB 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097
 RESULT 5
 ABZ13545
 ID ABZ13545 standard; DNA; 1026 BP.
 XX
 AC ABZ13545;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1350.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200216655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US026685.
 XX
 PR 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX
 DR WPI; 2002-304127/34.
 XX
 PT Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.

XX Claim 144; SEQ ID NO 1350; 577bp + Sequence Listing; English.

PS The invention relates to identifying a stress condition to which a plant

CC cell has been exposed, comprising: (a) contacting nucleic acid

CC representative of expressed polynucleotides in the plant cell with an

CC array or probes representative of the plant cell genome; and (b)

CC detecting a profile of expressed polynucleotides in the plant cell

CC characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants

CC with increased tolerance to abiotic stress. The present sequence is that

CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

CC in methods of the invention. Note: The sequence data for this patent is

CC not represented in the printed specification but is based on sequence

CC information supplied to Derwent by the European Patent Office

XX

SQ Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.39e-109	Length:	1026
Score:	1092.50	Matches:	210
Percent Similarity:	76.81%	Conservative:	45
Best Local Similarity:	63.25%	Mismatches:	72
Query Match:	62.50%	Indels:	5
DB:	6	Gaps:	3

US-10-670-454-2 (1-331) x ABZ13545 (1-1026)

QY 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18

DB 1 ATGGTGGTTTGGCCACAGCCAGCTCACTTAGATAAACCACTCTCCCTAATCCCCACATAC 60

QY 19 LysSerThrProLeuPheThr-----GlyLeProValValAspLeuThrHisProAsp 36

DB 61 AAACCGGTTCGGGTTCTCCCAATCAATCCCGTCGTCACCTAGCCGACCGGAA 120

QY 37 AlaLysAsnLeuLeuValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis 56

DB 121 GCGAAACCGGATCGTAAAGCGCTCGGAGAGTTGGGTTCTTCAAGGTGCTAAACAC 180

QY 57 GlyValProLeuLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys 76

DB 181 GGAGTCGACCGCAACTCATGACTCGGTAGAGCAGGAGCTATTGGCTTCTTCGGCTTG 240

QY 77 SerGlnSerGlyLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg 96

DB 241 CCTCAGTCCTTAAACACCGGCGCGTCCACCTGAACCGTACGGTTATGGTAAACCG 300

QY 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuAsnThrAsnProAsp 116

DB 301 ATTGGACCAACCGTGACGTTGGTTGGATTGAGTATCTCTCTCAATGCTAATCTCAG 360

QY 117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaVal 136

DB 361 CTCCTCTCTCTAAACCTCCGCGCGTTCTCCGTCAAACCCCTCAAAATTTTCGAGTGC 420

QY 137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla 156

DB 421 GTGGAGGAGTACATGAAGGAGATTAAAGGAGTTCGTACAAGGTGTGGAGATTGGTGC 480

QY 157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176

DB 481 GAAGAACTAGGATAGACCGACGACCTCTGAGTAAATGCTGAGATGAGAGAT 540

QY 177 AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196

DB 541 GACTCGTCTGAGACTAAACCATTTATCCGCGCGGAGGAA---GAGCGCGGAGAGATG 597

QY 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsn 216

DB 598 GTGAAGGTGGGGTTTGGGGAACACACAGACCCACAGATAATCTCAGTGTGAATCTAT 657

QY 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProAsp 236

DB 658 AACACGGCGGGTCTTCAAAATCTGTGTGAAGAAGATGGAAGTGGGTCTGCTCCTCCTGAT 717

QY 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256

DB 718 CACTCTCTCTTCTTCAATTAATGTGTGAGATGCTCTTCAGGTTATGACTAACGGAGGTTTC 777

QY 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276

DB 778 AGAGGTGTTAAACACAGGGTCTTAGCCGATACACAGGAGATCGAGGATTTCAATGATATAT 837

QY 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296

DB 838 TTTCGGCGGACCGCATTTGAGCCAGAAGATCGCACCATTCGCATTCCTTCTCCTGACCAA 897

QY 297 GluGluCysLeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSer 316

DB 898 GATGATTGGCTTTTACAAAGAAATTCATCTGCTCTCAATACAAATCTTCTCTTACAAGTCT 957

QY 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328

DB 958 AAGCTTGGTGATATAGACTTGGTCTCTTTGAGAAA 993

RESULT 6

ADA67975

ID ADA67975 standard; DNA; 1026 BP.

XX AC ADA67975;

XX DT 20-NOV-2003 (first entry)

XX DE Arabidopsis thaliana gene, SEQ ID 223.

XX KW Plant; bacterial infection; fungal infection; viral infection; ds.

XX OS Arabidopsis thaliana.

XX PN WO2003000898-A1.

XX PD 03-JAN-2003.

XX PF 22-JUN-2001; 2001WO-IB001105.

XX PR 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX DR WPI; 2003-175290/17.

XX PT Identifying at least one gene involved in plant resistance or response to

PT pathogenic infection for conferring resistance or tolerance to a plant to

PT bacterial, fungal or viral infection by determining or detecting plant

PT gene expression.

XX Claim 6; SEQ ID NO 223; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes

CC involved in plant resistance or response to pathogenic infection. M1

CC comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to

CC expression of the gene in an uninfected plant, in a mutant plant that

CC does not express a gene associated with response to pathogenic infection,

CC or in a corresponding incompatible or compatible interaction. (M1) is

CC useful for conferring resistance to resistance or tolerance to a plant to

CC bacterial, fungal or viral infection. The present sequence was used to

CC illustrate the invention.

SQ Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;

Alignment Scores:


```

Pred. No.: 7,39e-109 Length: 1026
Score: 1092.50 Matches: 210
Percent Similarity: 76.81% Conservative: 45
Best Local Similarity: 63.25% Mismatches: 72
Query Match: 62.50% Indels: 5
DB: 8 Gaps: 3

US-10-670-454-2 (1-331) x ADA67975 (1-1026)

Qy 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
Db 1 ATGGTGGTTTGGCCACAGCCAGTCATTTAGATAACCCATCTCCCTAATCCCCACATAC 60

Qy 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
Db 61 AAACCGGTTCCGGTTCTCCTACTTCCCATTCATCAATCCCGCTGCTCACTAGCCGATCCGAA 120

Qy 37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis 56
Db 121 GCGAAACCGGNAATCGTAAAGCCTGCGAGGAGTTCCGGTTCTTCAAGGTGTAACACAC 180

Qy 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys 76
Db 181 GGAGTCCGACCGAATCATGACTCGGTAGAGCAGAGGCTATTGGCTTCTTCGGCTTG 240

Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg 96
Db 241 CCTCAGTCTCTTAAACACCGGCGGTCACCTGAACCGTACGGTTATGGTAATAAAGCG 300

Qy 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAsp 116
Db 301 ATTGACCAAAACGGGTGAGCTGGTTGGATTGAGTATCTCTCTCAATGCTAATCTCAG 360

Qy 117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaVal 136
Db 361 CTCTCTCTCTTAAACCTCCGCGGTTTCCTGTAACCCCTCAATTTTCGGTACGTCG 420

Qy 137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla 156
Db 421 GTGAGGAGGATCATGAAGGAGATTAAGGAAGTGTCTACAGGTGTGGAGATGTTGCC 480

Qy 157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
Db 481 GAAGAACTAGGGATAGACCAAGGACACTCTCGAGTAAATCTCGAGATGAGAGAGT 540

Qy 177 AspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArg 196
Db 541 GACTGCTGCTGAGACTAAACCATTTATCCGGCGGCGGAGAA--GAGCGGAGAGATG 597

Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db 598 GTGAAGGTGGGTTTGGGGAACACACAGACCCACAGATAATCTCAGTGTCTAAGATCTAAT 657

Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAsp 236
Db 658 AACACGGCGGGTCTTCAATCTGTGTGAAGATGGAAGTTGGGTGCTGCTCCCTCAT 717

Qy 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 718 CACTCTCTCTTCTTCAATATGTTGAGATGCTCTTCAGGTATGACTAACGGGAGGTT 777

Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLysSerMetIleTyr 276
Db 778 AAGAGTGTAAACACAGGCTCTTAGCCGATACAGAGGATCGAGATTTCAATGATATAT 837

Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db 838 TTCGGCGGACCCCATTCAGCCAGAGATCGCACCATTCGATGCTGCTGCTCCCTGAGCA 897

Qy 297 GluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLeuAlaAlaThrSer 316
Db 898 GATGATTGGCTTTTCAAAAGATTCATCTGGTCTCAATCAATCTCTCTGCTTACAGTCT 957

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Qy 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 958 AAGCTTGGTATTAGACTTGGTCTCTTTGAGAA 993

RESULT 7
AAZ55916
ID AAZ55916 standard; cDNA; 1237 BP.
XX
AC AAZ55916;
XX
DT 10-APR-2000 (first entry)
XX
DE Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA.
XX
KW Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
growth inhibition; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 109..1134
FT /tag= a
FT /product= "Gibberellin 2-oxidase AtGA2ox2"
XX
FN WO9966029-A2.
XX
PD 23-DEC-1999.
XX
PF 11-JUN-1999; 99WO-GB001857.
XX
PR 12-JUN-1998; 98GB-00012821.
PR 15-JUL-1998; 98GB-00015404.
XX
PA (UYBR-) UNIV BRISTOL.
PI Thomas SG, Hedden P, Phillips AL;
XX
DR WPI; 2000-097742/08.
DR P-PSDB; AAY58599.
XX
PT New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
to produce transgenic plants with improved or altered growth
characteristics.
XX
PS Example 3; Fig 7; 42pp; English.
XX
CC This sequence represents cDNA encoding an Arabidopsis thaliana
gibberellin (GA) 2-oxidase, PGGA2ox2. This enzyme is a GA 2-beta-
hydroxylase that acts on G19-GAs and for which 2-beta-hydroxylation is
its only activity. Hydroxylation at the 2-beta position of a GA results
in a biologically inactive product, and is the most important route for
GA metabolism in plants, ensuring that the active hormones do not
accumulate in plant tissues. The nucleic acids can be used to transform
plants so that gibberellin 2-oxidase can be constitutively over-expressed
or otherwise enhanced to reduce the concentration of bioactive GA in the
plants and therefore to inhibit plant growth. Growth inhibition is useful
in many agricultural and horticultural applications such as enhancing
lodging-resistance and grain yield in cereals, improving seedling
quality, reducing the growth of amenity grasses, reducing shoot growth in
orchard and ornamental trees, improving tolerance to cold, drought and
infection, and increasing yields (by the diversion of assimilates from
vegetative to reproductive organs). The nucleic acids may also be used to
induce male and/or female sterility (by expression in floral organs),
prevent pre-harvest sprouting, reduce shoot growth in hedging plants,
inhibit reversibility in the development or germination of seeds and
reduce shoot growth in commercial wood species. Antisense constructs of
the nucleic acids can also be used to transform plants to reduce the
expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
improve fruit set and growth in seedless grapes, citrus fruits and
pears), improve skin texture and fruit shape in apples, increase stem
length and therefore yield in sugar cane, increase yield and earliness in
celery and rhubarb, improve malting yields and quality in cereals
(particularly barley), and increase growth in woody species

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XX SQ Sequence 1237 BP; 356 A; 277 C; 280 G; 324 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.66e-109	Length:	1237
Score:	1092.50	Matches:	210
Percent Similarity:	76.81%	Conservative:	45
Best Local Similarity:	63.25%	Mismatches:	72
Query Match:	62.50%	Indels:	5
DB:	3	Gaps:	3

US-10-670-454-2 (1-331) x ANZ555916 (1-1237)

Qy 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysPropHe 18
|||||
Db 109 ATGTGGTGTTCGCCACAGCCAGTCCTTTAGATAACCACATCTCCTTAATCCCCCACATAC 168
|||
Qy 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
|||||
Db 169 AAACCGGTTCGGGTTCACATTCCTCAATCCCCTCGTCGAACATAGCGCATCCGGAA 228
|||||
Qy 37 AlalysAsnLeuIleValAsnAlaCyArgAspPheGlyPhePheLysLeuValAsnHis 56
|||||
Db 229 GCGAAAACCCGAATCGTAAAGCCTGCAGGAGTTCGGTTCCTTCAGAGTCGTAAACAC 288
|||||
Qy 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPheLysLys 76
|||||
Db 289 GGAGTCGACCCGAACATCATGACTCGGTTAGACGAGGAGGCTATTGGCTCTCTCGGCTTG 348
|||||
Qy 77 SerGlnSerGluLysAspArgAlaGlyProAspProPheGlyTyrgLySerLysArg 96
|||||
Db 349 CCTCAGTCTCTTAAAAACCGCGCGTCCACCTGAACCGTACGGTTATGGTAATAAACGG 408
|||||
Qy 97 IleGlyProAsnGlyAspValGlyTrpValGluTyrlLeuLeuLeuAsnThrAsnProAsp 116
|||||
Db 409 ATTGGACCAACGGTGACGTGGTGGATTGAGTATCTCTCTCAATGCTAATCCTCAG 468
|||||
Qy 117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisShisPheArgAlaVal 136
:::
Db 469 CTCTCTCTCTCTAAAAACCTCGCGCGTTTTTCGCTCAAACCCCTCAAAATTTTCCGTCGAGTCG 528
|||||
Qy 137 ValGluAsnTyrlIleThraAlaValLysAsnMetCystYrAlaValLeuGluLeuMetAla 156
|||||
Db 529 GTGGAGAGTACATGAAGAGGATTAAGAAGTGTCTGACAAGTGTGTGGAGATGGTGTGCC 589
|||||
Qy 157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
|||||
Db 589 GAAGAACTAGGATAGACCAAGGACACTCTGAGTAAAAATGCTGAGAGATGAGAAGATG 648
|||||
Qy 177 AspSerCysPheArgLeuAsnHisTyrlProProCysProGluValGlnAlaLeuAsnArg 196
|||||
Db 649 GACTCTGCTCTGAGACTAAACCATTTATCCGCGCGCGGAGGAA---GAGCGCGGAGAGATG 705
|||||
Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
|||||
Db 706 GTGAAGGTGGGGTTGGGGAAACACAGACCACAGATAATCTCAGTGTCTAAGATCTAAT 765
|||||
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAsp 236
:::
Db 766 AACACGGCGGGTCTTCAAAATCTGTGTGAAGATGGAAGTTGGTGGTGGTCTCCTCTGAT 825
|||||
Qy 237 GlnThrSerPhePheIleAsnValGlyAspAlaIleuGlnValMetThrAsnGlyArgPhe 256
:::
Db 826 CACTCTCTCTTCTTCAATATGTTGGAGATGCTCTTTCAGGTTATGACTTAACGGGAGGTT 885
|||||
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrl 276
|||||
Db 886 AAGAGTGTAAACACAGGGTCTTAGCCGATCAAGAGATCGAGATTTCAATGATATAT 945
|||||
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
|||||
Db 946 TTCGGCGACCGCATTTGAGCAGAGATCGCACTTGCATGCTGCTGTCCCTCGAGCAA 1005

3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein HVMR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter. The nucleic acid fragments may be used to create transgenic plants where the polypeptides are present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally found. The polynucleotides can be used as probes for genetically and physically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length polymorphism (RFLP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used as hybridisation probes against PCR amplification products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. Antibodies are useful for detecting the polypeptides in situ in cells or in vitro in cell extracts. The present sequence encodes a plant metabolism protein (or fragment).

XX Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.53e-106 Length: 1352
Score: 1068.50 Matches: 201
Percent Similarity: 77.95% Conservative: 57
Best Local Similarity: 60.73% Mismatches: 68
Query Match: 61.13% Indels: 5
DB: 12 Gaps: 2

US-10-670-454-2 (1-331) x ADM94213 (1-1352)

Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLeuPhePheLeuSer 20
Db 159 ATGGTGTGGTGGTCCAAAGCAACAAACAGAACAAATCTCTCATTAAGCAATGCATGCCA 218
Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLeuAsnLeu 40
Db 219 ACCAAATTTCTCAACAAATTTCCCATATGAGACCTCTCCAAACCTGATGCAAGACCTT 278
Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
Db 279 ATAGTGAAGCTTGTGAGGAGTTGGATCTTCAAGATCATCAATCATGGTGTCTCCATG 338
Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLeuLeuSerGlnSerGlu 80
Db 339 GAAGCTATATCCGAATTCGAATATGAGCCTTCAAAATTCCTCTCATGCTCAATGAA 398
Qy 81 LysAspArgAlaGlyProAspPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 399 AAGGAAAGTAGGACCTCCCAATCCATTTGGTATGGTAGCAAGAAATTCGACACAA 458
Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 459 GGGGAGGTGGTGGATGGTGGTACCTCTCTCAACACCAATCAAGAA----- 506
Qy 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 507 CACAACCTCTCTGTTTATGGGAAAAACCCCTGAGAAATTCAGGTGTCTGTGAACAGTTAC 566
Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 567 ATGCTCTCTGGAGGAAGATGGCATGTGAGATCTTGTAGTTGATGGCAGAGGGTTGAAG 626
Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 627 ATTCAGCAAAAGGATGTGTTTAGCAAGCTTCTAATGGATAAACAAGTACTCTATTTC 686
Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200

Db 587 AGGTGAATCATTTACCTGCTTGTCTCGAATGACTCTGATGATGATCAGAACTTGATTGGG 746
Qy 201 PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly 220
Db 747 TTTGGAGAACACACACAGACCCCAAAATCATCTCTCTGTTAAGATCCAAACACTTCAGGC 806
Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 240
Db 807 CTTTCAAGATTTATCTTAGAGATGGAAATTTGGATTTTCAAGTCCACACAGATGACAAATCCTTT 866
Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 867 TTTATTAACGTGTGTGATCTCTTCAGGTATGACAAATGGAAGTTCGGAAGTGTGAGA 926
Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 927 CACAGAGTGTGGCAAAATGGGTTTCAAGTCCAGGCTTTCAATGATTTACTTTGGAGGTCCA 986
Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
Db 987 CTTTGTAGTGAAGAAATAGCACCATTTATCTCTCTCATG---AAAGGAAAGAAAGTCTA 1043
Qy 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 1044 TATAAAGAGTTTACTCTGTTTGGATACAAATAATCAATCTACGTTCAAGATTATCTAAA 1103
Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 1104 AATAGACTTTGAACATTTTGAAGAAGATTCAGCT 1136
RESULT 9
ADM94205
ID ADM94205 standard; cDNA; 1365 BP.
XX
AC ADM94205;
XX 17-JUN-2004 (first entry)
XX
DE Soybean Dioxygenase cDNA #1.
XX
KW Soybean; ss; plant; plant metabolism;
KW GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase;
KW Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase;
KW Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;
KW Ethylene response factor; Acyl-CoA thioesterase II;
KW ABC transporter GCN20-like; P-glycoprotein I; P-glycoprotein 3;
KW P-glycoprotein ATPGP; P-glycoprotein HVMR2; ABC transporter;
KW PMP70 ABC transporter; MRP4 ABC transporter; transgenic.
XX
OS Glycine max.
XX
FN US6677502-B1.
XX
PD 13-JAN-2004.
XX
PF 12-JUL-2000; 2000US-00614912.
XX
PR 12-JUL-1999; 99US-0143401P.
PR 12-JUL-1999; 99US-0143412P.
PR 30-JUL-1999; 99US-0146650P.
PR 15-DEC-1999; 99US-0170906P.
PR 21-DEC-1999; 99US-0172946P.
PR 21-DEC-1999; 99US-0172959P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
PI Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Pang Y;
PI Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
PI Li CP;
XX WPI; 2004-088430/09.

DR P-PSDB; ADM94206.
 XX New isolated GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate
 PT synthase nucleic acid and proteins, useful for creating transgenic plants
 PT where polypeptides are present at higher or lower levels.
 XX
 PS Example 3; SEQ ID NO 5; 186pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising a
 CC nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
 CC II/3, 4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as
 CC ADM94266. Also included are a vector comprising the polynucleotide, a
 CC recombinant DNA construct comprising the polynucleotide operably linked
 CC to at least one regulatory sequence, transforming a cell with the
 CC polynucleotide, a cell comprising the recombinant DNA construct,
 CC producing a plant (comprising transforming a plant cell with the
 CC polynucleotide and regenerating a plant from the transformed plant cell),
 CC a plant comprising the recombinant DNA construct and a seed comprising
 CC the recombinant DNA construct. Also disclosed as new are nucleic acid
 CC (cDNA) fragments and assembled contigs encoding plant metabolism proteins
 CC chosen from GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate
 CC synthase, dioxynase, Ent-kaurane Synthase A, GA-20 oxidase, Gibberellin
 CC 3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
 CC factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-
 CC glycoprotein 1, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein
 CC HvMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
 CC The nucleic acid fragments may be used to create transgenic plants where
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or in developmental stages in which they are not normally
 CC found. The polynucleotides can be used as probes for genetically and
 CC physically mapping genes and as markers for traits linked to those genes.
 CC The nucleic acid fragments may be used as restriction fragment length
 CC polymorphism (RFLP). It can also be used to probe Southern blots
 CC containing restriction endonuclease-treated genomic DNAs of a set of
 CC individuals representing parent and progeny of a defined genetic cross.
 CC The nucleic acid fragments may also be used as hybridisation probes
 CC against PCR amplification products generated from the mutation population
 CC using the mutation tag sequence primer in conjunction with an arbitrary
 CC genomic site primer. The peptides can also be used to immunise animals to
 CC produce polyclonal or monoclonal antibodies with specificity for peptides
 CC or proteins comprising the amino acid sequences. Antibodies are useful
 CC for detecting the polypeptides in situ in cells or in vitro in cell
 CC extracts. The present sequence encodes a plant metabolism protein (or
 CC fragment).
 XX
 SQ Sequence 1365 BP; 448 A; 258 C; 244 G; 415 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3, 42e-105 Length: 1365
 Score: 1060.50 Matches: 200
 Percent Similarity: 77.64% Conservative: 57
 Best Local Similarity: 60.42% Mismatches: 69
 Query Match: 60.67% Indels: 5
 DB: 12 Gaps: 2

US-10-670-454-2 (1-331) x ADM94205 (1-1365)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
 DB 166 ATGGTGTGTGTCCTCAAGAACCAACAGAACATACTCTTACATTAAAGAACTGCATGCCA 225
 QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 DB 226 ACCAAATTTTCTCAACAATTCCTAGTAGGACCTCTCCAAACCTGATGCAGACCCCTT 285
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 DB 286 ATAGTGAAGGCTGTGAGGAGTTTGATTTCTTCAAAGTCATCAATCATGTGTCTCCATG 345
 QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
 DB 346 GAAGCTATATCCGAATTGGAATATGAAGGCTTCAAATTTCTTCTATGTCACCTCAATGAA 405

QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
 DB 406 AAGGAAAAAGTAGGACCTCCCAATCCATTGGGTATGGTAGCAGAAAAATTCGACACAT 465
 QY 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValLysPro 120
 DB 466 AGGACGTTGGTGGATTGATGATCTTCTTCAACACCAATCAAGAA----- 513
 QY 121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
 DB 514 CCAACTTCTCTGTTATGGCAAAACCTGGAATTCAGGTGTCTGTGTGACAGTTAC 573
 QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
 DB 574 ATGTCTTCTGTGAGCAAGATGTCATGTGAGATTCTTGTGATGTCAGCAAGGGTTGAAG 633
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 DB 634 ATTCAAGCAAAAGGATGTGTTTAGCAAGCTTCTTAATGGATTAACCAAGTGACTCTATTTC 693
 QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
 DB 694 AGGGTGAATCATTAACCTGCTTGTCTGAAATGACTCTCAATGATCAGAACTTGATGGG 753
 QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
 DB 754 TTTGAGAAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCAAACACACTTCAGGC 813
 QY 221 LeuGlnIleCysLeuThrAspGlyThrTyrValSerValProAspGlnThrSerPhe 240
 DB 814 CTTCAAGATTATCTTAGAGATGGAATTTGATTTTCCAGTCCCAACAGATCAAAATCCTTT 873
 QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
 DB 874 TTTATTACGTTGGTGATCTCTTCAAGTTATGACAAATGAAGGTTCCGAAGTGTGAGA 933
 QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
 DB 934 CACAGAGTGTGGCAAAATGGGTTCAAGTCCAGCTTTCATGATTTTACATTTTGGAGGTCCA 993
 QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
 DB 994 CCTTTGAGTGAATAATAGCACCATTTATCTCTCTCATG---AAAGGAAAGAAAGTCTTA 1050
 QY 301 TyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
 DB 1051 TATAAAGATTACTGTTGGTTGAGTACAAAAAATCAATCTACGTTCAAGATTATCTATA 1110
 QY 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
 DB 1111 AATAGACTTGAACATTTTGAAGAATTGCACT 1143
 RESULT 10
 AAZ99472
 ID AAZ99472 standard; cDNA; 1403 BP.
 XX AAZ99472;
 XX 03-JUL-2000 (first entry)
 DT Soybean gibberellic acid 2-oxidase 2 cDNA sequence.
 DE
 XX Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; ss.
 XX Glycine max.
 XX Key Location/Qualifiers
 FT 149..1129
 CDS /*tag= a
 FT /product= "gibberellic acid 2-oxidase 2"

XX PS Claim 6; SEQ ID NO 3443; 899pp; English.

XX CC The present invention relates to a method (M1) for identifying genes

CC involved in plant resistance or response to pathogenic infection. M1

CC comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to

CC the incompatible interaction of plant gene expression relative to

CC expression of the gene in an uninfected plant, in a mutant plant that

CC does not express a gene associated with response to pathogenic infection,

CC or in a corresponding incompatible or compatible interaction. (M1) is

CC useful for conferring resistance to resistance or tolerance to a plant to

CC bacterial, fungal or viral infection. The present sequence was used to

CC illustrate the invention.

XX SQ Sequence 984 BP; 165 A; 311 C; 341 G; 167 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7,33e-96	Length:	984
Score:	973.00	Matches:	190
Percent Similarity:	72.67%	Conservative:	52
Best Local Similarity:	57.06%	Mismatches:	79
Query Match:	55.66%	Indels:	12
DB:	8	Gaps:	3

US-10-670-454-2 (1-331) x ADA70120 (1-984)

QY 1 MetValValLeuSer---GlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLys 19

DB 1 ATGGTGGTTCTGCTGCGCCGCGCGCGTGCATCATCCCGCTGCTGAGGTGCGCGGAC 60

QY 20 SerThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysAsn 39

DB 61 CCGCGGACGCTCTTCCGCGGTGCGCGTGCAGCTCGCGACGCCCGCGCGCGCGGAG 120

QY 40 LeuLeuValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59

DB 121 GCGGTGGTGGAGCGCTCGCGAGCGGTACAGGTCTTCAAGGTGCTCAACACCGCGGTGGCC 180

QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79

DB 181 ACGACACATGACACAGCGCGAGTCCGAGGCGGTCTTCTCCAGACGACGCGCC 240

QY 80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgLleGlyPro 99

DB 241 GACAGGACCGCTCCGCGCGCGCTACCGTTCGCGGTACGCGACGAGCGGATCGGGTTC 300

QY 100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsn-----Pro 115

DB 301 AATGGCGACATGGGTGGTTCGAGTACCTCTCTCGCCCTCGACGACGCGCTCGCTCGCC 360

QY 116 AspValLleSerProLysSerLeuCysLlePheArgGluAsnProHisPheArgAla 135

DB 361 GACGCTGCACCGTCCGCTCTGCGCGGTCT-----TTCCGGGCGC 399

QY 136 ValValGluAsnTyrLleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMet 155

DB 400 GCTCTCAACGAGTACATCTCGCGGGTGCAGAGGTGCGGTGATGAGGCGGATG 459

QY 156 AlaGluGlyLeuGlyLleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLys 175

DB 460 TCGGAGGGGTGGGCAATTCGCGAGGCGGACGCGCTGAGCGCGCTGATGACGCGGAGGG 519

QY 176 SerAspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsn 195

DB 520 ACGGACAGGTGTTCCGCGTGAACCACTACCGCGCTGCGCGGTGCGGGCTCGGC 579

QY 196 ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnLleLleSerValLeuArgSer 215

DB 580 TGCAGGCTCACCGGCTTCGCGGAGCACACCGACCGCGAGCTCGTCTCGCTCGCTCA 639

QY 216 AsnSerThrSerGlyLeuGlnLleCysLeuThrAspGlyThrTrpValSerValProPro 235

DB 640 AACGGCACGCTCGCGCTGAGATCGCGCTCCGCGAGCGCGAGTGGGTGTCCTGCGCCCTCC 699

QY 236 AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg 255

DB 700 GACCGCGACTCTCTTCTCAACGTCGCGACTCGTTGCGAGTTCTGACCAATGGGAGG 759

QY 256 PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetLle 275

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QY 276 TyrPheGlyGlyProAlaLeuSerGluAsnLleAlaProLeuProSerValMetLeuLys 295

DB 820 TACTTTGGAGGCGCCACCGTTAGCACAGGATTGCACCATGCCACAGCTGCTGGGGAG 879

QY 296 GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaLalaLysThr 315

DB 880 GGAGAGCAGAGCGCTGTCAAGGAGTTTCAATGGGATGAGTACAGAGGCTGCCTACAAA 939

QY 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328

DB 940 TCAAGGCTTGGAGACACACAGGCTGGCCCGCAGTTTGAGAAAG 978

RESULT 13

ADK00081

ID ADK00081 standard; cDNA; 984 BP.

XX AC ADK00081;

XX DT 17-JUN-2004 (first entry)

XX DE Rice cDNA encoding gibberellin 2-oxidase, OsGA2ox3.

XX KW Rice; ss; gene; plant; gibberellin 2-oxidase; OsGA2ox3; plant growth; gibberellin A20; gibberellin A29; gibberellin A29-catabolite.

XX OS Oryza sativa.

XX FH Key

FT CDS 1..984

FT Location/Qualifiers

FT /tag= a

FT /product= "OsGA2ox3"

XX US2004060080-A1.

XX PD 25-MAR-2004.

XX PF 18-MAR-2003; 2003US-00392325.

XX PR 20-SEP-2002; 2002JP-00276051.

XX PA (NAG-) NAT INST AGROBIOLOGICAL SCI.

XX PI (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

XX PI Tanaka H, Kayano T, Matsuoka M, Kobayashi M, Saito T, Sakamoto T; Sakai M;

XX WPI; 2004-268919/25.

XX P-PSDB; ADK00082.

XX New DNA encoding plant-derived proteins having gibberellin 2-oxidation activity, useful for the inactivation of plant gibberellins and plants whose gibberellin activity has been modified by regulating the expression of these DNAs.

XX Claim 1; SEQ ID NO 3; 23pp; English.

XX The invention relates to a DNA encoding a plant protein having gibberellin 2-oxidation activity, comprising ADK00079 or ADK00081 or a DNA encoding a protein comprising ADK00080 or ADK00082, where one or more amino acid residues are substituted, deleted, added, and/or inserted or a DNA hybridising to ADK00079 or ADK00081 under stringent conditions. The DNA is also selected from an antisense RNA, a DNA encoding an RNA having the ribozyme activity that specifically cleaves the transcript of the DNA above, a DNA encoding an RNA that suppresses the expression of the DNA

above in plant cells via RNAi, or a DNA encoding an RNA that suppresses the expression of the DNA above in plant cells by co-suppression. Also included are a protein encoded by the DNA above, a vector harbouring a DNA selected above, a transformed plant cell harbouring the DNA above or the vector, a transgenic plant comprising the transformed plant cell or is an offspring or clone of the transgenic plant, a propagation material obtained from the transgenic plant, a method of producing a transgenic plant, a plant growth suppressor comprising the DNA above as an active ingredient, a method of suppressing plant growth and a method of promoting plant growth. The gibberellin 2-oxidase catalyses the conversion of gibberellin A20 to gibberellin A29, which is further metabolised to gibberellin A29-catabolite. The DNAs are useful in the inactivation of plant gibberellins and plants whose gibberellin activity has been modified by regulating the expression of these DNAs. The present sequence encodes gibberellin 2-oxidase, OsGA2ox3.

SQ Sequence 984 BP; 165 A; 311 C; 341 G; 167 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.33e-96	Length:	984
Score:	973.00	Matches:	190
Percent Similarity:	72.67%	Conservative:	52
Best Local Similarity:	57.06%	Mismatches:	79
Query Match:	55.66%	Indels:	12
DB:	12	Gaps:	3

US-10-670-454-2 (1-331) x ADK00081 (1-984)

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 DB 1 ATGTGGTTCCTCGTCCCGCGCGCGCTGCATCATCATCCGCTGCTGAGTCCGCGAC 60
 QY 20 SerThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsn 39
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 QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
 DB 121 GCCGTGGTGGACGCTCGAGCGGTACGGGTCTTCAAGTCTGCAACACCGCGTGGCC 180
 QY 60 LeuGluLeuMetAlaLeuLeuGluAenGluAlaLeuArgPhePheLysLysSerGlnSer 79
 DB 181 ACGGACACGATGATGACAAAGGCGGAGTGGAGCGCTCAGGTCTCTCCACGACGACGCC 240
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 QY 100 AsnGlyAspValGlyTrpValGluTyrrLeuLeuLeuAsnThrAsn-----Pro 115
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 QY 116 AspValIleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAla 135
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 QY 136 ValValGluAsnTyrrIleAlaValLysAsnMetCysTyrrAlaValLeuGluLeuMet 155
 DB 400 GCTCTGAACGAGTACATCTCGGGGTGCGGAAGTGGCGGTGGGTGATGAGGCGGATG 459
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 DB 460 TCGGAGGGCTGGCATTTGGCAGCGGACGCGCTGAGCGGTGGTGGCGGGAAGG 519
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 DB 520 AGCGACACGATGTTCGCGGTGAACCACTACCCCGCTGCGCGCTGACGGGCTCGGC 579
 QY 196 ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleSerValLeuArgSer 215
 DB 580 TGGAGGCTACCCGCTTCGCGGAGCACACCGACCGGAGCTGCTCCGCTCCGCTCA 639
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DB 640 AACGGCACGTCGCGCTGCAGATCGGCTCCGCGACGCGCAGTGGGTGTCGCTCCCTCC 699
 QY 236 AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg 255
 DB 700 GACCGGATCTCTCTTCGTCACGTCGCGGACTCGTTCGAGGTCTTGACCAATGGAGG 759
 QY 256 PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle 275
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 QY 276 TyrPheGlyGlyProAlaLeuSerGluAenIleAlaProLeuProSerValMetLeuLys 295
 DB 820 TACTTTGGAGGGCCACCGTTAGCACAGAGGATTGCACCATTCGCACAGCTGCTGGGGAG 879
 QY 296 GlyGluGluCysLeuTyrrLysGluPheThrTrpCysGluTyrrLysLysAlaIleThr 315
 DB 880 GGAGAGCAGACGCTGTACAGGAGTTTCATCATGGGATGATACAGAAAGCTGCCTACAA 939
 QY 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
 DB 940 TCAGGCTTGGAGACACAGCGCTGGCCCGCAGTTTGAGAG 978
 RESULT 14
 AEB67784
 ID AEB67784 standard; DNA; 1271 BP.
 XX AC AEB67784;
 DT 22-SEP-2005 (first entry)
 XX DE Rice genome derived DNA sequence, SEQ ID 2929.
 XX KW transcription; gene regulation; transgenic plant; RNA interference;
 XX transformation; antibody; ds.
 OS Oryza sp.
 XX JP2005185101-A.
 XX PD 14-JUL-2005.
 XX PF 11-DEC-2002; 2002JP-00383870.
 XX PR 30-MAY-2002; 2002JP-00203269.
 XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 XX PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
 XX PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
 XX PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
 XX PI Kikuchi H, Hayashizaki Y, Ootomo Y, Matsubara K, Murakami K;
 XX PI Kishimoto N, Sato K, Nagata T, Kawakami N, Yazaki J, Ishikawa M;
 XX PI Doi K, Kawai J;
 XX DR WPI; 2005-566181/58.
 XX PT Novel DNA encoding transcription factor, derived from rice plant, useful
 PT for obtaining transcriptional-regulatory regions in plant and for
 PT producing modified plant.
 XX PS Claim 1; SEQ ID NO 2929; 2928pp; Japanese.
 CC The invention relates to a novel DNA sequence encoding a transcription
 CC factor derived from a plant. The invention further comprises antisense
 CC RNA sequences, ribozyme activity RNA, RNAi sequences, a vector,
 CC transformed plant cells, antibodies and proteins, all related to the
 CC novel plant DNA sequences of the invention. The novel DNA is preferably
 CC derived from a rice-genome database. The invention further provides a
 CC method for determining the transcription regulatory regions of the rice
 CC genome. The novel DNA is useful for controlling the expression of a gene
 CC in a plant and for producing a modified plant with desired and different
 CC characteristics. The plant DNA and method enables the acquisition of many

CC polynucleotide, a cell comprising the recombinant DNA construct,
 CC producing a plant (comprising transforming a plant cell with the
 CC polynucleotide and regenerating a plant from the transformed plant cell),
 CC a plant comprising the recombinant DNA construct and a seed comprising
 CC the recombinant DNA construct. Also disclosed as new are nucleic acid
 CC (cDNA) fragments and assembled configs encoding plant metabolism proteins
 CC chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
 CC synthase, Dioxynase, Ent-kaurane Synthase A, GA-20 oxidase, Gibberellin
 CC 3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
 CC factor, Acyl-CoA thioesterase II, ABC transporter GGN20-like, P-
 CC glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein
 CC HMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
 CC The nucleic acid fragments may be used to create transgenic plants where
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or in developmental stages in which they are not normally
 CC found. The polynucleotides can be used as probes for genetically and
 CC physically mapping genes and as markers for traits linked to those genes.
 CC The nucleic acid fragments may be used as restriction fragment length
 CC polymorphism (RFLP). It can also be used to probe Southern blots
 CC containing restriction endonuclease-treated genomic DNAs of a set of
 CC individuals representing parent and progeny of a defined genetic cross.
 CC The nucleic acid fragments may also be used as hybridisation probes
 CC against PCR amplification products generated from the mutation population
 CC using the mutation tag sequence primer in conjunction with an arbitrary
 CC genomic site primer. The peptides can also be used to immunise animals to
 CC produce polyclonal or monoclonal antibodies with specificity for peptides
 CC or proteins comprising the amino acid sequences. Antibodies are useful
 CC for detecting the polypeptides in situ in cells or in vitro in cell
 CC extracts. The present sequence encodes a plant metabolism protein (or
 CC fragment).

XX

SQ Sequence 1650 BP; 353 A; 463 C; 476 G; 358 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,54e-95	Length:	1650
Score:	973.00	Matches:	190
Percent Similarity:	72.67%	Conservative:	52
Best Local Similarity:	57.06%	Mismatches:	79
Query Match:	55.66%	Indels:	12
DB:	12	Gaps:	3

US-10-670-454-2 (1-331) x ADM94203 (1-1650)

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QY	20	SerThrProLeuPheThrGlylleProValValAspLeuThrHisProAspAlaLysAsn	39
DB	188	CCCGGCGACGCTCTCTCCGCGGTGCGCGTGTGTCGACCTCGGCAGCCCGCGCGGAGG	247
QY	40	LeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValPro	59
DB	248	GCGTGTGGACCGCTCGCGAGCGGTACGGGTCTTCAAGTGTCAACACCGCGCGGCGC	307
QY	60	LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer	79
DB	308	ACGACACGATGGACAAAGCCGAGTCGAGGCGGTCTCTTCTCCACGACGACGCC	367
QY	80	GluLysAspArgAlaGlyProProAspPropheGlyTyrGlySerLysArglleGlyPro	99
DB	368	GACAGGACCGCTCCGCGCGCGCTACCCGCTTCGGGTAGCGCAGCAAGCGGATCGGGTTC	427
QY	100	AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuLeuAsnThrAsn-----Pro	115
DB	428	AATGGCGACATGGGGTGGGTGAGTAGCTACCTCTCGCCCTCGACGCGCTGCTCGCC	487
QY	116	AspValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAla	135
DB	488	GAGCGCTGCACCGCTCCGCTCTCGCGGTC-----TTCCGGGCGC	526
QY	136	ValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMet	155

DB	527	GCTCTGAACAGAGTACATCTCGGGGGTGCAGAAAGTGGCGGTGATGGAGGCGATG	586
QY	156	AlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLys	175
DB	587	TGGAGGGGCTGGGCATTCGGCAGCGGACGGCTGAGCGCTGTGTGACGGCGAAGGG	646
QY	176	SerAspSerCysPheArgLeuLeuAsnHisTyrProCysProGluValGlnAlaLeuAsn	195
DB	647	AGCGACCAAGTGTTCGCGGTGAACCACTACCCGCGGTGCGCGCGCTCGCGCTCGGC	706
QY	196	ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSer	215
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QY	216	AsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProPro	235
DB	767	ACGGCACGCTCGGCCCTGCAGATCGCGCTCCGGCAGCGCAGTGGGTGTCCGTGCCCTCC	826
QY	236	AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg	255
DB	827	GACCGCGACTCTCTTCTTCTCAACGTCGCGGACTCGTTGACGTTCTGACCAATGGAGG	886
QY	256	PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle	275
DB	887	TTCAAGAGCGTGAAGCACAGGCTGGTGGCCACAGCCTAAAGTCTAGGGTTTCTTCATC	946
QY	276	TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys	295
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QY	296	GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaIleTyrThr	315
DB	1007	GGAGAGCAGAGCTGTACAAAGGAGTTTCATCGGATGAGTACAAAGAGGCTGCCTACAA	1066
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4	1065.5	61.0	1363	4	CNSOABKL	BX815974 Arabidops
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6	957.5	54.8	1554	4	AY104425	Zea mays
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Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M., URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full_length

<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

FEATURES

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Location/Qualifiers

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Best Local Similarity: 63.25% Mismatches: 72
Query Match: 62.50% Indels: 5
DB: 4 Gaps: 3

US-10-670-454-2 (1-331) x CNSOBSJ (1-1362)

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QY 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
DB 162 AAACCGGTTCGGTCTTCACCTCCCATTCATCCCGTGTCAACTAGCGAGTCCGGAA 221
QY 37 AlaLysAsnLeuLeValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis 56
DB 222 GCGAAACCGAATCGTAAAGCGTCGAGGAGTTCGGGTCTTCAAGTCTGTAACCCAC 281
QY 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys 76
DB 282 GGAGTCCGACCGCACTCATGACTCGGTAGACGAGGAGCTATTGGCTTCTTCGGCTTG 341
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DB 342 CCTCAGTCTCTTAAACCGCGCGGTCCACCTGAACCGTACGGTTATGGTAATAAACGG 401
QY 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuAsnThrAsnProAsp 116
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QY 117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaVal 136
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ORGANISM
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REFERENCE
1 (bases 1 to 1365)
Castelli V., Aury J.M., Jallion O., Wincker P., Clepet C.,
Menard M., Cruaud C., Quetier F., Scarpelli C., Schachter V.,
Temple G., Caboche M., Weissenbach J. and Salanoubat M.
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 1365)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full_length
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ORIGIN

Alignment Scores:
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Percent Similarity: 76,81% Conservative: 45
Best Local Similarity: 63,25% Mismatches: 72
Query Match: 62,50% Indels: 5
DB: 4 Gaps: 3

US-10-670-454-2 (1-331) x CNS0AC6N (1-1365)
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Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyGlySerLysArg 96
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Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
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Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuMetIleTyrl 276

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CNS0AC3R 1339 bp mRNA linear HTC 06-FEB-2004
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BX814383.1 GI:42472054
HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

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REFERENCE
AUTHORS
1 (bases 1 to 1339)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche M., Weissenbach,J. and Salanoubat M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 1339)
Genoscope.
Direct Submission
JOURNAL
TITLE
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.
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217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAsp 236
 760 AACACGGCGGCTTCAATCTGTGTGAAGATGGAAGTTGGTCTCGCTCCCTCCTGAT 819

237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
 820 CACTCTCTCTTCTTCAATTAATGTTGAGATGCTTTCAGGTTATGACTAACGGGAGTTTC 879

257 LysSerValLysHisArgValLeuAlaAspThrLysSerArgLeuSerMetIleTyr 276
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297 GluGluCys-----LeuTyrLysGluPheThrTrpCysGluTyr 309
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 VERSION AY104425.1 GI:21207503
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 Clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1554)
 Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H.,
 Fang,Z., Morgante,M., Landewe,T., Fengler,K., Uebeche,F.,
 Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H.
 Jr.
 Anchoring 9,371 maize expressed sequence tagged unigenes to the
 bacterial artificial chromosome contig map by two-dimensional
 overgo hybridization
 Plant Physiol. 134 (4), 1317-1326 (2004)
 15020742
 2 (bases 1 to 1554)
 Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
 Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
 Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)

REFERENCE 3 (bases 1 to 1554)
 COE,E.H.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 COMMENT
 If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB, and may be found by BLAST
 searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.
 FEATURES
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US-10-670-454-2 (1-331) x AY104425 (1-1554)
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018_5_05_018, mRNA sequence.
ACCESSION
AJ803092
VERSION
AJ803092.1 GI:51118420
KEYWORDS
EST.
SOURCE
Antirrhinum majus (snapdragon)
ORGANISM
Antirrhinum majus
REFERENCE
1 (bases 1 to 785)
Bey.M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
TITLE
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL
Plant Cell 16 (12), 3197-3215 (2004)
PUBMED
15539471
COMMENT
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
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Db 371 AACTTAATCGGGTTTTGGTGAACATACTACCCGCAATAATATCCGTTTTTGAGATCCCAAC 430
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAsp 236
Db 431 AACACTTCGGGTCTTCAAAATTCGTTGAAGATGGGAATGGGATTTCTATCCACTGAT 490
Qy 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 491 CAAAGTCTCTTCTTCATTAATGTTGCTGACTCCTGCTGAGGTTATGACTAATGGCAGGTTT 550
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
Db 551 AAGAGTGTGAAGACAGAGGTTGTGGCCCAACAGCTCAAAACCCAGACTTTTCAATGATATAT 610
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db 611 TTGGAGGACCCACCAATTAAAGTGAAGATAGCTCCATTCCTTCAGTACTAATGAAGA 670
Qy 297 GluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLeuAlaLysThrSer 316
Db 671 GAAGACAGCTTGTCAAGGAATTTACTTGGTTTGAGTACAAAAAATCTGCTTATAATCAA 730
Qy 317 ArgLeuAlaAspAsnArg 322
Db 731 GGCTGGCTGATAATAGG 748

RESULT 9
DN589159 893 bp mRNA linear EST 15-MAR-2005
LOCUS
DEFINITION
50141.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
50141_5', mRNA sequence.
ACCESSION
DN589159
VERSION
DN589159.1 GI:61239615
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 893)
Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De
Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)
COMMENT
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.
FEATURES
Location/Qualifiers
1..893
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"

```


/clone="50141"
 /tissue_type="Tubers"
 /lab_host="XL10-Gold"
 /clone_lib="Late Blight-Challenged Tubers"
 /note="Vector: pBluescript II SK(+); XR: Site 1: EcoRI;
 Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
 from pathogen-free Solanum tuberosum var. Shepody, clone
 1756, were inoculated with 5 ul of Phytophthora infestans
 (A2-mating type), through 2 puncture wounds 3 cm apart.
 The tubers were incubated 1 minute to allow inoculum
 absorption. The infection area was outlined for future
 collection reference. Surface slices were sampled from the
 tubers at 1 day, 5 days, 7 days, 11 days and 14 days
 post-infection. All samples were pooled and used for RNA
 isolation and library construction. A normalized library
 was constructed following a modified protocol of Bonaldo
 et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-91 Length: 893
 Score: 868.50 Matches: 168
 Percent Similarity: 79.92% Conservativeness: 27
 Best Local Similarity: 68.85% Mismatches: 46
 Query Match: 49.69% Indels: 3
 DB: 8 Gaps: 3

US-10-670-454-2 (1-331) x DN589159 (1-893)

QY 88 AspProPheGlyTyrGlySerIysArgIleGlyProAsnGlyAspValGlyTyrValGlu 107
 DB 3 GACCCCTTTGGCTATGGAATAAGAAATGGACCTAATGGTGGTGGTGGTGGTAA 62
 QY 108 TyrLeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArg 127
 DB 63 TACATCTTTTGTCACAAATTCGAGTTCATTAACCAAAATTTGTCATCTATTGGGT 122
 QY 128 GluAsnProHisPheArgAlaValValGluAsnTyrIleThrAlaValIysAsnMet 147
 DB 123 GTCATCCAAAAGATATAGAGATGCTGTGAATGATTATGATTAGCAATGAAGAAATG 182
 QY 148 CysTyrAlaValLeuLeuLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeu 167
 DB 183 GCTTGTGAGATTCTTGAATCTTTAGCAGAGGATTAATAATTCATCCAAAGAATGTATT 242
 QY 168 SerArgLeuLeuAspGlyLysSerAspSerCysPheArgLeuAsnHisTyrProPro 187
 DB 243 AGTAAGCTTTTAATGGATGAAATAAGTGAATTCATCTTTTAGGCTAAATCATTTACCTCCA 302
 QY 188 CysPro---GluValGlnAlaLeuAsn---ArgAsnLeuValGlyPheGlyGluHisThr 205
 DB 303 TGTCTGTGATGATTTCAAGAAATATAATGCAAGAAATTTAATTTGGATTGTCGACATCT 362
 QY 206 AspProGlnIleSerValLeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeu 225
 DB 363 GATCCACAAATATTCTTTTATAGATCAATCAACACTCTCGACTCTCAAAATTTCACTT 422
 QY 226 ThrAspGlyThrTyrValSerValProAspGlnThrSerPhePheIleAsnValGly 245
 DB 423 GTTGATGGCCATGGATTCTGTCCCACTGATCAAAATTCATCTTCATCAATGTGTGT 482
 QY 246 AspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValIysHisArgValLeuAla 265
 DB 483 GATTCAATCCAGGTGATGACAAATGGAGGTTTAAGAGTGTAACATAGATTGTCGCC 542
 QY 266 AspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyProAlaLeuSerGluAsn 285
 DB 543 AATAGTGTAAATCAAGACTCTCAATGATTTATTTTGGAGGGGCCCATTTAGTGAAGAAG 602
 QY 286 IleAlaProLeuProSerValMetLeuLysGly---GluGluCysLeuTyrLysGluPhe 304
 DB 603 ATAGCACCATTTGTCATCTATTATAATAAAGGGGATCAAGACGCTGTACAAAGAATTT 662

QY 305 ThrTrpCysGluTyrLysAlaAlaTyrThrSerArgLeuAlaAspAsnArgLeuAla 324
 DB 663 ACATGGTTTGATCAAAAATTCAGCATATAAATTCAGATTGGCTGATAATAGGTGGTC 722
 QY 325 PropheGlnLys 328
 DB 723 CTATTTTGAGAA 734

RESULT 10

BI935635

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Seq primer: T3.

Location/Qualifiers

1. .792

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CTOD23D23"

/tissue_type="flower"

/dev_stage="anthesis"

/clone_lib="tomato flower, anthesis"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; supplier: Cornell University; sequencing: The

Institute for Genomic Research; Flower buds and flowers

were taken from greenhouse plants (4-8 wks old, TA496).

They were immediately frozen in liquid nitrogen and then

size-separated while remaining frozen."

ORIGIN

Alignment Scores:

Pred. No.: 4.62e-88 Length: 792

Score: 837.00 Matches: 158

Percent Similarity: 73.53% Conservativeness: 42

Best Local Similarity: 58.09% Mismatches: 56

Query Match: 47.88% Indels: 16

DB: 3 Gaps: 2

US-10-670-454-2 (1-331) x BI935635 (1-792)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLysProPheLysSer 20

DB 12 ATGGTGATCTTGCC-----AAACAA 32

QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40

DB 33 ACCTCATCTTTTAATGGTGTTCATTGATTGACCTCTCTAAACCCGACTCCCAAGAACCTC 92

QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuAsnHisGlyValProLeu 60


```
Db      93  ATCGTTAATGCTCCGCGAAGAAATTCGGATTCTTCAAAATCATAAACACCATGACGTTCCTATG 152
QY      61  GluLeuMetAlaAenLeuGluAenGluAlaLeuArgPhePheLysSerGlnSerGlu 80
Db      153 GAATTCATAGTAATCGAATCCGAGCCATCAGTCTTCTCCTCCCTCTCTGAG 212
QY      81  LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db      213 AAGCTAAAGCAGGCGCTGCTGATCCTTTGGCTATGGCAATAAACAATTCGAACAAT 272
QY      101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAenThrAsnProAspValIleSerPro 120
Db      273 GCGGATTGTGTCGGTCCGACACATCTCGTATTCGACAAATTCGAAATCAATTACCAG 332
QY      121 LysSerLeuCysIlePheArgGluAenProHisPheArgAlaValValGluAenTyr 140
Db      333 AATTGTGATCTATATAGTGTCATCCGAAACATTCGGGCTCGGCTTAAATGATTAT 392
QY      141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db      393 GTTTCAGCAGTGAAGAAATGCTCTGTGATATTTCTTGAAATGTTGGCGGAGGATTAAAG 452
QY      161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db      453 ATTATCCGACGAATCTTTTCAGTAAGCTTTTGATGACGAAATAGCAGCTCCGTTTTC 512
QY      181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAenArgAsn----- 197
Db      513 AGCTGAATCAGTATCCGATCTCAGAGATTTGAACGATTGACGATTAATATATGAT 572
QY      198 LeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSer 217
Db      573 TTGATTGGATTGGAGAACATCTGACCCACCAATCATATCGATATTAAGATCCATAAC 632
QY      218 ThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGln 237
Db      633 ACTTCGGGGCTCCAAATATTACTGAAGATGGACACTGGATCTCTGCCACCTCGATGAA 692
QY      238 ThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLys 257
Db      693 AATCTCTTCTGTCATGTGTGACTCATTCAGGTTATGACTAACGGAAGGGTTAAG 752
QY      258 SerValLysHisArgValLeuAlaAspThrThrLys 269
Db      753 AGTGTGAAGCATAGGTATTGGGCAATAGTGTGAAA 788

RESULT 11
BM085298
LOCUS
DEFINITION
  saj34h07.y1 Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID:
  Gm-c1066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ; mRNA
  sequence.
ACCESSION
  BM085298.1 GI:16995926
VERSION
  EST.
KEYWORDS
  Glycine max (soybean)
ORGANISM
  Glycine max
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
  Glycine.
  1 (bases 1 to 566)
REFERENCE
  Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvett, V.,
  Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
  Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
  Bowers, J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
  Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
  McCann, R., Waterston, R. and Wilson, R.
  Public Soybean EST Project
  Unpublished (1999)
  Contact: Shoemaker R/Public Soybean EST Project
  Public Soybean EST Project
  Washington University School of Medicine
```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 426.

FEATURES

source
1..566
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1066-4957"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week
old seedling"
/lab_host="DH10B"
/clone_lib="Gm-c1066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedling from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

ORIGIN

Alignment Scores:
Pred. No.: 7,3e-87 Length: 566
Score: 825.00 Matches: 159
Percent Similarity: 89.62% Conservative: 5
Best Local Similarity: 86.89% Mismatches: 19
Query Match: 47.20% Indels: 0
DB: 3 Gaps: 0
US-10-670-454-2 (1-331) x BM085298 (1-566)
QY 1 MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLysProPheLysSer 20
Db 18 ATGGTTGTTTGTCTCAGCCAGCATTAACACAGTTTTTCTCTGAAAAACATGCAAGCCC 77
QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 78 ACGCCCTCTTCTCCGGGATTCGCTGGTGGACCTCACGACCCCGATGCCAAGACCCAC 137
QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 138 ATAGTGAAGCCTCGAGGAGCTTCGGCTTCTTCAGCTCGTGACACACCGTGTTCATT 197
QY 61 GluLeuMetAlaAsnLeuGluAenGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 198 GAGTTCATGGCCAAATTTGAAAAACCCCTCAGGTCTTCAAAAAACCTCAGTCCGAC 257
QY 81 LysAspArgAlaGlyProProAspProPheGlyPhePheLysLeuValAsnHisGlyValProAsn 100
Db 258 AAAGACAGGCTGGTGGTCCCTCATCTTTTGGCTACGGCAGCAGAGGATTGGCCCTAAC 317
QY 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAenThrAsnProAspValIleSerPro 120
Db 318 GCGGATGTCGGTGGTTCGAATACCTCTTCTCAACACCAACCTGACCTCATCTCCCC 377
QY 121 LysSerLeuCysIlePheArgGluAenProHisHisPheArgAlaValValGluAenTyr 140

Db 378 AGTCACTGATTTCCGAGAAAGTCTCAGAAATTCAGGGTGTCTTGGAGGATAC 437
 QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
 Db 438 ATTAGAGCGCTGAGAACATGTCTATGAGTGTGGAATTAATGCGGAGGGCTTGGGA 497
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 Db 498 ATAACCTCAGAGGAATCGTTGAGTAGTGTCTGCTGAGGATGAGAAGAGTGATCTTGTCTTC 557
 QY 181 ArgLeuAsn 183
 Db 558 AGACTTAAC 566

RESULT 12

AW184969 653 bp mRNA linear EST 24-JUL-2004
 LOCUS se84f09.y1 Gm-cl023 glycine max cdna clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-cl023-1410 5' similar to TR:004162 004162 DIOXYGENASE. ;, mRNA
 sequence.

ACCESSION

VERSION AW184969

KEYWORDS

SOURCE EST

ORGANISM

Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 653)
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Other ESTs: BU544870 corresponding to Gm-r1088-979 (3')
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. This clone is
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
 Insert Length: 1472 Std Error: 0.00

High quality sequence stop: 436.

FEATURES

source

1. .653
 /location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="T157"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl023-1410"
 /tissue_type="seed coats of greenhouse grown plants"
 /lab_host="DH10B"
 /clone_lib="Gm-cl023"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
 cdna library was constructed from mRNA isolated from seed
 coats (100-200mg) of greenhouse grown plants. The
 library was prepared using the Life Technologies
 SuperScript cdna library construction kit. Complimentary
 DNA was synthesized from mRNA using a poly (dT) sequence
 with a Not I restriction site. Sal I linkers adapters
 were ligated to the blunt-ended cdna fragments followed by
 Not I digestion. The cdna fragments were directionally
 cloned into the Not I-Sal I restriction site of the
 pSPORT1 vector. The ligated cdna fragments were

transformed into E.coli Electromax DH10B host cells. This
 library was constructed by Dr. Lila Vodkin and Dr. Anu
 Khanna."

ORIGIN

Alignment Scores:
 Pred. No.: 8,096-86 Length: 653
 Score: 817.00 Matches: 158
 Percent Similarity: 84.74% Conservatives: 3
 Best Local Similarity: 83.16% Mismatches: 29
 Query Match: 46.74% Indels: 0
 DB: 1 Gaps: 0

US-10-670-454-2 (1-331) x AW184969 (1-653)

QY 1 MetValValLeuSerGlnProAlaLeuAanGlnPhePheLeuLysProPheLysSer 20
 Db 84 ATGGTTGTTCTGTCTCAGCCAGCATTAACCAAGTTTTTCTTCTGANAACATGCAAGCCC 143
 QY 21 ThrProLeuPheThrGlyLeProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 Db 144 ACGCCCTTGTTCGGCGGGGATTCTCTGTGTCGACCTCAGGACCCCGATGCCAAGACCCAC 203
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 Db 204 ATAGTCAATGCTCAGGAGACTTCGGCTTCTTCAAGCTCGTGAACACCGTGTTCGGTTA 263
 QY 61 GluLeuMetAlaAsnLeuGluAanGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
 Db 264 CAGTTCATGGCCCAATTTGGAAACCAACCCCTCGGGTCTTCAAAAACCTCAATCCGAG 323
 QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgileGlyProAsn 100
 Db 324 AAAGACAGGGCTGGTCCCTGACCTTTCGCTACGGCAGCAGAGGATTCGCCCTAAC 383
 QY 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAanThrAsnProAspValLysSerPro 120
 Db 384 GCGCATGTGCGTGGGTGGAATACCTCTCTTCAACCAACCAACCTCATCTCCCCC 443
 QY 121 LysSerLeuCysIlePheArgGluAanProHisPheArgAlaValValGluAanTyr 140
 Db 444 AAGTCACATGTCATTTTCAGAAAGGTCCTCAGAAATTTTCANGCGGTGTGGAGGAATAC 503
 QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
 Db 504 ATTAGAGCGGTGAAGACATGTGCTATGAGGTGTGGAATTCATGCTCANGGATTGTGG 563
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSerAspSerCysPhe 180
 Db 564 ATAACGCATAGGAATGTGTGAGTATGTTGCTGAACGATGAGAAGAGTGATCTTGTCTTC 623
 QY 181 ArgLeuAanHisTyrProProCysProGlu 190
 Db 624 AGACNTTACCCTACCCGCCCATTCGCCGAT 653

RESULT 13

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BI208568 694 bp mRNA linear EST 11-JUL-2001
 EST526608 cTOS Lycopersicon esculentum cdna clone cTOS17020 5' end,
 mRNA sequence.

BI208568

BI208568.1 GI:14686292

EST.

Lycopersicon esculentum (Solanum lycopersicum)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 694)

van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,

Ronning, C. and Tanksley, S.

Generation of ESTs from Tomato Suspension Cultures

Unpublished (2001)


```

COMMENT      Contact: CUGI
              Clemson University Genomics Institute
              100 Jordan Hall, Clemson, SC 29634, USA
              Email: http://www.genome.clemson.edu/orders/index.html.

FEATURES
  source     1..694
             /organism="Lycopersicon esculentum"
             /mol_type="mRNA"
             /cultivar="FA496, B6203"
             /db_xref="taxon:4081"
             /clone="cFOS17020"
             /tissue_type="suspension cultures"
             /lab_host="SOLR"
             /clone_lib="cTOS"
             /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
             XhoI; Suspension cultures of L.esculentum E6203 were grown
             in Murashige and Skoog based medium, supplemented with 15%
             coconut milk (filter sterilized and added after
             autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).
             Fresh medium was added every 7 days, and cultures were
             grown at 25 C, with 12hrs of light and continuous
             shaking."

ORIGIN
Alignment Scores:
  Pred. No.:      3 49e-85      Length:      694
  Score:          812.00      Matches:     152
  Percent Similarity: 80.95%      Conservative: 35
  Best Local Similarity: 65.80%      Mismatches:  42
  Query Match:    46.45%      Indels:      2
  DB:             2           Gaps:         2

US-10-670-454-2 (1-331) x B1208568 (1-694)

Qy  91  GlyTyrGlySerLysArgIleGlyProAsnGlyAspValGlyTrpValGluTyrLeuLeu 110
Db  3  GGTATGGCAATAAGAAAATCGACAAAATGGCGATATCGTTGGTGTGAATACATTCTC 62

Qy  111 LeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsnPro 130
Db  63  CTTTCAACAAATCTGAATCAATACCAGAAATTCGCATCTGTATATAGGTGTCATATCCA 122

Qy  131 HisHisPheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAla 150
Db  123 GAAACATTCGGGCTCGGTGATGATGATGTCATCATCAGTGAAGAAAATGTATCTGAG 182

Qy  151 ValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeu 170
Db  183 ATTCTGMAAAGTTGGCGGAGGGATTAAGATTCACCCGACGAATGTTTGTAGTAAGCTA 242

Qy  171 LeuLysAspGluLysSerAspSerCysPheArgLeuAsnHisTyrProProCysProGlu 190
Db  243 TTGATGATGAAAAGACGCACTCTGTTTTCAGGCTGAATCAGTATCTCTCCATGTCCTGAT 302

Qy  191 ValGlnAlaLeuAsn--ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIle 209
Db  303 ATTCAGAATTTCATGCCAAAATTTAATGGATTTGGAGAACATATCTGATCCACAAATC 362

Qy  210 IleSerValLeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThr 229
Db  363 ATGTCGATTTTAAAGATCCAAACACACTTCGGTCTTCAAAATTTACTCAAAAATGCGAAC 422

Qy  230 TrpValSerValProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGln 249
Db  423 TGGTTTCTGTTCCATCTGATCAGAAATCTTTTTTCGTCATGTTGGAGACTCATTTACAG 482

Qy  250 ValMetThrAsnGlyArgPheLysSerValLysHisArgValLeuAlaAspThrThrLys 269
Db  483 GTGATGACGATGGAAGTTTATAGATGTGAACATAGGGTGTGACAAACAGCTGTGAAA 542

Qy  270 SerArgLeuSerMetIleTyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeu 289

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RESULT 14
BW690134 755 bp mRNA linear EST 27-APR-2005
LOCUS BW690134 Lycopersicon esculentum cv. Micro-Tom fruit Lycopersicon
DEFINITION esculentum CDNA clone FCI7CG04 5', mRNA sequence.
ACCESSION BW690134 GI:62932545
KEYWORDS EST.
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 755)
AUTHORS Tsugane,T., Watanabe,M., Yano,K., Suzuki,H., Sakurai,N. and
Shibata,D.
TITLE Expressed sequence tags of full-length cDNA clones prepared from
the laboratory-grown miniature tomato (Lycopersicon esculentum)
cultivar Micro-Tom
JOURNAL Unpublished (2005)
COMMENT Contact: Daisuke Shibata
Kazusa DNA Research Institute;
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3947
Fax: 81-438-52-3948
Email: shibata@kazusa.or.jp.
FEATURES
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US-10-670-454-2 (1-331) x BW690134 (1-755)

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Qy  41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
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Qy  61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db  158 GAATTCATAAGAACTCGAATCCGAAGCCATCAAGTTCTTCTCTCTCTCTCTCTCTCTGAG 217

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2005, 01:23:14 ; Search time 249 Seconds
(without alignments)
2362.943 Million cell updates/sec

Title: US-10-670-454-2

Perfect score: 1748

Sequence: 1 MVVLSQPALNOFFLLKPKFS.....AAYTSRLADNRLAPPQKSA 331

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Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Issued Patents NA:

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SUMMARIES

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3	1092.5	62.5	1237	3	US-09-719-108-7		Sequence 7, Appli
4	1068.5	61.1	1352	3	US-09-614-912-13		Sequence 13, Appl
5	1060.5	60.7	1365	3	US-09-614-912-5		Sequence 5, Appli
6	1060	60.6	1403	3	US-09-371-307-64		Sequence 64, Appl
7	973	55.7	1650	3	US-09-614-912-3		Sequence 3, Appli
8	972	55.6	1473	3	US-09-614-912-7		Sequence 7, Appli
9	957.5	54.8	1555	3	US-09-614-912-1		Sequence 1, Appli

10	953	54.5	1008	3	US-09-719-108-9	Sequence 9, Appli
11	936.5	53.6	1318	3	US-09-719-108-5	Sequence 5, Appli
12	746	42.7	783	3	US-09-371-307-57	Sequence 67, Appl
13	661	37.8	966	3	US-09-371-307-58	Sequence 58, Appl
14	553	31.6	811	3	US-09-371-307-71	Sequence 71, Appl
15	442.5	25.3	406	3	US-09-371-307-68	Sequence 68, Appl
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ALIGNMENTS

RESULT 1
US-09-719-108-1
; Sequence 1, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-09-719-108-1

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QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
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; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
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; ORGANISM: Glycine max
; US-09-371-307-62

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Query Match: 87.1% Indels: 1
DB: 3 Gaps: 1

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US-09-719-108-7
 ; Sequence 7, Application US/09719108
 ; Patent No. 6670527
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Stephen G
 ; APPLICANT: Hedden, Peter
 ; APPLICANT: Phillips, Andrew L
 ; TITLE OF INVENTION: Gibberellin 2-Oxidase
 ; FILE REFERENCE: 0623.0970000
 ; CURRENT APPLICATION NUMBER: US/09/719,108
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: PCT/GB99/01857
 ; PRIOR FILING DATE: 1999-06-11
 ; PRIOR APPLICATION NUMBER: GB 9812821.8
 ; PRIOR FILING DATE: 1998-06-12
 ; PRIOR APPLICATION NUMBER: GB 9815404.0
 ; PRIOR FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 16
 ; SEQ ID NO 7
 ; LENGTH: 1237
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-719-108-7

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 Query Match: 62.50% Indels: 5
 DB: 3 Gaps: 3

US-10-670-454-2 (1-331) x US-09-719-108-7 (1-1237)

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 QY 77 SerGlnSerGluLysAspArgAlaGlyProProAspPropheGlyTyThrGlySerLysArg 96
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 QY 137 ValGluAsnTyIleThrAlaValLysAsnMetCysTyAlaValLeuGluLeuMetAla 156
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 QY 157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
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 Db 649 GACTCGTCTGAGACTAAACCATTCCTCGCGCGCGGAGGAA---GAGCGGAGAGATG 705
 QY 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
 Db 706 GTGAAGTGGGTTTGGGGAACACACACACACACACACACACACACACACACACACACAT 765
 QY 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAsp 236
 Db 766 AACACGCGGGTCTTCAAAATCTGTGAAAGATGGAAGTGGGTCGCTGTCTCCTCTGAT 825
 QY 237 GlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
 Db 826 CACTCTTCTTCTTCAATTAATGTTGGAGATGCTCTTCAGGTTATGACTAACGGAGGTT 885
 QY 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTy 276
 Db 886 AAGAGTGTAAACACAGAGGCTCTTAGCCGATACAGAGGATCGAGGATTTCAATGATAT 945
 QY 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
 Db 946 TTCGGCGGCGCCATTGAGCCAGAAAGATCGCACCATTTGCCATGCTTGTCTCCTGAGCAA 1005
 QY 297 GluGluCysLeuTyLysGluPheThrTrpCysGluTyLysLysAlaAlaTyThrSer 316
 Db 1006 GATGATTGGCTTTACAAAGAAATTCATTTGGTCTCAATACAAATCTTCTGCTTACAGTCT 1065
 QY 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
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RESULT 4

US-09-614-912-13
 ; Sequence 13, Application US/09614912
 ; Patent No. 6677502
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Miao, Gou-Hau
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Lee, Jian Ming
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Weng, Zude


```
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-13

Alignment Scores:
Pred. No.: 7,49e-121 Length: 1352
Score: 1068.50 Matches: 201
Percent Similarity: 77.95% Conservative: 57
Best Local Similarity: 60.73% Mismatches: 68
Query Match: 61.13% Indels: 5
DB: 3 Gaps: 2

US-10-670-454-2 (1-331) x US-09-614-912-13 (1-1352)

QY 1 MetValValSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer 20
DB 159 ATGGTGTTCCTCCAAAGCAACACAGAACAAATACCTCTACATTAAGAACTGCATGCCA 218
QY 21 ThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysLeu 40
DB 219 ACCAAATTTCTCAACAATTCCTAGTAGGACCTCTCCAAACCTGATCCAAAGACCCCTT 278
QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
DB 279 ATAGTGAAGCTTGTCAGAGATTGGATTCTTCAAGTCATCATCATGTTCTCCATG 338
QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
DB 339 GAAGCTATATCCGAATTGGAATATGAAGCTTCAAAATCTCTCTATGTCACCTCAATGAA 398
QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
DB 399 AAGGAAAAAGTAGGACCTCCCAATCCATTTGGTATGGTAGCAAGAAAAATTGGACACAA 458
QY 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
DB 459 GGGGAGCTTGGTGGATTGAGTACCTCTCTCAACACCAATCAAGAA----- 506
QY 121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
DB 507 CACAACCTCTCTGTTTATGGGAAAAACCTCGAGAAATTCAGGTGTCGTGTGAACAGTTAC 566
QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
DB 567 ATGCTCTCTGTGAGGAAGATGGCATGTGAGATTCTTGAAGTGTGATGTCAGAGGGTTGAAG 626
QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
DB 627 ATTCAGAAAAGAGATGTTTACAGAGCTTCTTAATGGAATAAACAAGTACTCTATTTC 686
QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
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Db 687 AGGGTGAATCATTACCCTCTGTCTGCTGAATGACTCTGAATGATCAGAACTTGATTGGG 746
QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
DB 747 TTTGGAGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCCAACACACTTCAGGC 806
QY 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
DB 807 CTTTCAGATTATCTTAGAGATGGAATTTGGAATTCAGTCCCACAGATGACAAATCCTTT 866
QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
DB 867 TTTATTAACTGGTGGATTCTCTTCAGGTATGACAAATGGAAGGTTCGAAAGTGTGAGA 926
QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
DB 927 CACAGAGTGTGGCAAAATGGGTTCAAGTCCAGCTTCAATGATTACTTTGAGGTCCA 986
QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
DB 987 CCTTTGAGTGAGAAATAGCACCATATCTCTCTCATG--AAAGGAAAAGAAAGTCTTA 1043
QY 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
DB 1044 TATAAAGAGTTTACCTGTTGAGTACAAAAAATCAATCTACGGTTCAAGATTATCTATAA 1103

RESULT 5
US-09-614-912-5
; Sequence 5, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-5

Alignment Scores:
Pred. No.: 7,29e-120 Length: 1365
Score: 1060.50 Matches: 200
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Db 1111 AATAGACTTGAACATTTTGAAGAAGAAATTCAGCT 1143

RESULT 6

US-09-371-307-64

Sequence 64, Application US/09371307A

Patent No. 6723897

GENERAL INFORMATION:

APPLICANT: Brown, Sherri M.

APPLICANT: Heck, Gregory R.

APPLICANT: Piller, Kenneth J.

APPLICANT: Kishore, Ganesh M.

APPLICANT: Ellich, Tedd D.

APPLICANT: Logusch, Eugene W.

APPLICANT: Rao, Sudabathula

APPLICANT: Ream, Joel E.

APPLICANT: Logusch, Sherry J.

TITLE OF INVENTION: Methods for controlling gibberellin levels

FILE REFERENCE: MOBT-216

CURRENT APPLICATION NUMBER: US/09/371.307A

CURRENT FILING DATE: 1999-08-10

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 64

LENGTH: 1403

TYPE: DNA

ORGANISM: Glycine max

US-09-371-307-64

Alignment Scores:

Pred. No.:	8.77e-120	Length:	1403
Score:	1060.00	Matches:	200
Percent Similarity:	76.44%	Conservative:	53
Best Local Similarity:	60.42%	Mismatches:	72
Query Match:	60.64%	Indels:	6
DB:	3	Gaps:	3

US-10-670-454-2 (1-331) x US-09-371-307-64 (1-1403)

Qy	1	MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db	149	ATGGTGTGGTCTGCCAAGGCAACACAGAACATCTCTACATCAAGAACTACATGCCA 208
Qy	21	ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db	209	ACGGCATCTCTCCACAAATTCCTCGTAGTGAGACTCTCCAAACACAGATGCCAAGACCCTC 268
Qy	41	IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db	269	ATAGTAGAGGCTTGTGAGAAATTTGGATCTTCAAGTCATCAACCATGGTGTTCCCATG 328
Qy	61	GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db	329	GAACATATATCCCAATTTGGAATCTGAAGCCTTCAAGTTCTTCTCTATGCCACTCAATGAG 388
Qy	81	LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db	389	AAGGAAAAAGTAGGCCCTCCCAAAACCATATATGGGTATGGTAGCAAGAAAAATTGGACACAT 448
Qy	101	GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db	449	GGGGATGTGTGGTGGGTGAGTAGCTTCTTCTCAACCAATCAAGAA----- 496
Qy	121	LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db	497	CACAACCTTCTGTTTATGGCAAAAACCGCTGAGAAATTTAGGTGTTGTTGAACAGTTAC 556
Qy	141	IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluClyLeuGly 160
Db	557	ATGTCTTCTGTGAGCAAAATGGCATATGGAGATTCTTGAGCTGATGGCAGAGAGATTGAAG 616
Qy	161	IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db	617	ATACACAAAAAATGTGTTTAGCAAGCTTCTTATFGAATAAGAGAGTAGTCTGTTTT 676

QY 181 ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
 Db 677 AGGTGAATCACTACCTGCTGCTCCCTGACCTI--GTGAATGGTCAAAACATGATAGG 733
 QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
 Db 734 TTGGAGAACACACGGACCCACAAATCAATTTCTCTACTTAGGTCCAAATACTTCAGGC 793
 QY 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
 Db 794 CTTCAAGATTTTCTTAGAGATGGAATTCGATTTAGTCCCACTGATCACAATCTTTTC 853
 QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
 Db 854 TTCATTAATGTTGGTGATTTCTCTAGGTATATGACCAATAGGAAGTTTCGATGTGAAA 913
 QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
 Db 914 CACAGAGTTTTCACAAATAGATTTAAGTCTAGACTCTCAATGATTTTACATTTTGGAGTCCA 973
 QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
 Db 974 CCATTGAGTGAGAAAATAGTACCATTTATCTTCACTTATG--AAAGAAAAGAAAGCTTA 1030
 QY 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
 Db 1031 TACNAAGATTTACGTGGTTCGNGTATAAAATTTAACCTATGCTTCAAGATTGGCTGAT 1090
 QY 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
 Db 1091 AATAGGCTTGGACATTTTCAGAGAAATTTGGTCT 1123

RESULT 7

US-09-614-912-3
 ; Sequence 3, Application US/09614912
 ; Patent No. 6677502
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Miao, Gou-Hau
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Lee, Jian Ming
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Weng, Zude
 ; APPLICANT: Calimi, Perry G
 ; APPLICANT: Anderson, Shawn
 ; TITLE OF INVENTION: Plant Metabolism Genes
 ; FILE REFERENCE: BB1378 US NA
 ; CURRENT APPLICATION NUMBER: US/09/614,912
 ; CURRENT FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,401
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,412
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/146,650
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 60/170,906
 ; PRIOR FILING DATE: 1999-12-15
 ; PRIOR APPLICATION NUMBER: 60/172,959
 ; PRIOR FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: 60/172,946
 ; PRIOR FILING DATE: 1999-12-21
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 3
 ; LENGTH: 1650
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 US-09-614-912-3
 Alignment Scores:

Pred. No.: 5,39e-109 Length: 1650
 Score: 973.00 Matches: 190
 Percent Similarity: 72.67% Conservative: 52
 Best Local Similarity: 57.06% Mismatches: 79
 Query Match: 55.66% Indels: 12
 DB: 3 Gaps: 3
 US-10-670-454-2 (1-331) x US-09-614-912-3 (1-1650)
 QY 1 MetValValLeuSer---GlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLys 19
 Db 128 ATGGTGGTTCCTCGCTGGCCCGCCGCTCGATACATCCCTGCTGAGGTGCGCGAC 187
 QY 20 SerThrProPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsn 39
 Db 188 CCGCGGCGAGCTCTTTCGGCGGTGCGGTCGTCGACCTCGGCGAGCCCGCGCGCGAGG 247
 QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
 Db 248 GCGTGGTGGAGCGCTTCGAGCGGTACGGGTCTTCAAGGTCTTCCAGCGCGCTGGGC 307
 QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
 Db 308 ACGGACACGATGGACAAGCGCGAGTCGGAGCGGTCTTCTCCAGACGCGAGCCC 367
 QY 80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyPro 99
 Db 368 GACAGGACCGCTCGGCCCGCCCTACCGTTCGGGTACGCGACGAGCGGATCGGGTTC 427
 QY 100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsn-----Pro 115
 Db 428 AATGGCGACATGGGTGGTTCGAGTACCTCTCTCTCGCCCTCGACGCGCTCGCTCGCC 487
 QY 116 AspValIleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAla 135
 Db 488 GACGCTCGACCGTCCCGTCTCGCGGTC-----TTCGGGCGC 526
 QY 136 ValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMet 155
 Db 527 GCTCTGAACGATACATCTCGGGGGTGGCGAGGTGGCGGTGATGAGGCGATG 586
 QY 156 AlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLys 175
 Db 587 TCGAGGGGCTGGGCATTCGCGAGCGGACGCGCTGAGCGCTGTGACGCGGGAAGG 646
 QY 176 SerAspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsn 195
 Db 647 AGCGACCAAGTTCGCGTGAACCACTACCGCGCGTCCGCGCGCTCGAGGGGCTCGGC 706
 QY 196 ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleLysSerValLeuArgSer 215
 Db 707 TGCAGGTCACCGGCTTCGCGAGGACACCGACCGCGAGCTCGTCTCGTCCGCTCA 766
 QY 216 AsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProPro 235
 Db 767 AACGGCACGTCCGCGCTGCAGATCGCGCTCCGCGAGCGGCGAGTGGGTGCTCGCTCC 826
 QY 236 AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGluValMetThrAsnGlyArg 255
 Db 827 GACCGCGACTCTTCTTCAACGTCGGCGACTCGTTCAGGTTCCTGACCAATGGAGG 886
 QY 256 PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle 275
 Db 887 TTCAGAGGCTGAAGCACAGGGTGGTGGCCACAGCGCTAAGTCTAGGTTTCTTTCATC 946
 QY 276 TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys 295
 Db 947 TACTTTGGAGGGCCACCGTTAGCACAGAGGATTCACCATTCGACAGCTGCTGGGGAG 1006
 QY 296 GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysAlaAlaTyrThr 315
 Db 1007 GGAGAGCAGAGCTGTATCAAGGAGTTTCATGGGATGATGATCAAGAAGGCTGCCTCAAA 1066

QY 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
 Db 1067 TCAAGCCTTGGAGACAACAGCGTGGCCCGCCAGTTTGAGAG 1105

RESULT 8

US-09-614-912-7
 ; Sequence 7, Application US/09614912
 ; Patent No. 6677502
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Miao, Gou-Hau
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Lee, Jian Ming
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Weng, Zude
 ; APPLICANT: Caimi, Perry G
 ; APPLICANT: Anderson, Shawn
 ; TITLE OF INVENTION: Plant Metabolism Genes
 ; FILE REFERENCE: BB1378 US NA
 ; CURRENT APPLICATION NUMBER: US/09/614,912
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,401
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,412
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/146,650
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 60/170,906
 ; PRIOR FILING DATE: 1999-12-15
 ; PRIOR APPLICATION NUMBER: 60/172,959
 ; PRIOR FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: 60/172,946
 ; PRIOR FILING DATE: 1999-12-21
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 7
 ; LENGTH: 1473
 ; TYPE: DNA
 ; ORGANISM: Triticum aestivum
 US-09-614-912-7

Alignment Scores:

Pred. No.: 5,97e-109 Length: 1473
 Score: 972.00 Matches: 194
 Percent Similarity: 72.64% Conservative: 45
 Best Local Similarity: 58.97% Mismatches: 86
 Query Match: 55.61% Indels: 4
 DB: 3 Gaps: 3

US-10-670-454-2 (1-331) x US-09-614-912-7 (1-1473)

QY 1 MetValValLeu---SerGlnProAlaLeuAnGlnPhePheLeuLeuLysProPheLys 19
 Db 124 ATGGTGGTCTCGCAGCAGCGCCGCGTCGATCATCCCGCTCTCGCGCGCCGAC 183
 QY 20 SerThrProLeuPheThrGlyLeProValValAspLeuThrHisProAspAlaLysAsn 39
 Db 184 CCGGGGACTACTTCTCGGCGATCGGCGTGGTGGACCTCTCCAGCCCTGCGCGCGCGCGG 243
 QY 40 LeuLeValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
 Db 244 GCCATCGCGCGCGTGGCGGCTTCGGGTTCTTCAAGCTGTCACACCGGGGTGCC 303
 QY 60 LeuGluLeuMetAlaAsnLeuGluAnGluAlaLeuArgPhePheLysLysSerGlnSer 79
 Db 304 GCGACACGATGACAGCGTTCGAGTCGAGCGCGTCAGGTTCTTCTCGCTCGCGCGCGCC 363
 QY 80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgGlyGlyPro 99
 Db 364 GCAAGGACCGCTCGCGCGCGCGCTACCGGTTTCGCTGCGGACGAGCGATCGGCTC 423

QY 100 AsnGlyAspValGlyTyrValGluTyrLeuLeuLeuAnThrAsnProAspValLysSer 119
 Db 424 AATGGCAGCATGGGGTGGCTCGAGTACTGTCTCTCGCGCGTC-----GACTCCCGCTCG 477
 QY 120 ProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAn 139
 Db 478 CTCCTCGCGCGCTGGCGGTC---CCGTCTCGCGCGCTCTTCGCGCGCGCTGAACGAG 534
 QY 140 TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeu 159
 Db 535 TACATCGCGCGCGTGGCGGAGTGGCGGTGGTGGAGCGATGCGCGAGGCGGTG 594
 QY 160 GlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCys 179
 Db 595 GGCATTCGCGCGCTGGACGCTGAGCGGATGGTGGACGCGCGCGGAGCGGACGAGGTG 654
 QY 180 PheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAnArgAsnLeuVal 199
 Db 655 TTCGGGTGAACCACTACCCGCGTGCACGCGTGCAGGGGCTGGGCTGCAGCGCCACC 714
 QY 200 GlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSer 219
 Db 715 GCTTCGCGCGAGCACACGACCCGCGCTCATCTCGGTGCTCGCTCCAAACGCGACGCTCC 774
 QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProAspGlnThrSer 239
 Db 775 GGCCTGCAGATCGCGCTCCAGAACGCGGAGTGGGTGCTCGCTCGGACCGCGACGCGC 834
 QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
 Db 835 TTCCTGTCACAGTTCGCGGACTCGTTGCAAGTGTGTCACACGCGGAGGTTCAGAGCGTG 894
 QY 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
 Db 895 AAGCACAGGTTGGTGGCCACACAGCCTAAAGTCTAGGTGTTTCCATCATCTTCTTGAGG 954
 QY 280 ProAlaLeuSerGluAnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
 Db 955 CCAGCGATGACACAGAGATTGACCATTTGCGCGAGCTGTGCGGCGCGGAGAGAGAGC 1014
 QY 300 LeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAla 319
 Db 1015 CTGTACAAGGACTTCACATGGGCGAGTACAGAGGCTGCTCACTCCAGGCTCGGG 1074
 QY 320 AspAsnArgLeuAlaProPheGlnLys 328
 Db 1075 GACAACAGCTGGCTCAGTTCACAGG 1101
 RESULT 9
 US-09-614-912-1
 ; Sequence 1, Application US/09614912
 ; Patent No. 6677502
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Miao, Gou-Hau
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Lee, Jian Ming
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Weng, Zude
 ; APPLICANT: Caimi, Perry G
 ; APPLICANT: Anderson, Shawn
 ; TITLE OF INVENTION: Plant Metabolism Genes
 ; FILE REFERENCE: BB1378 US NA
 ; CURRENT APPLICATION NUMBER: US/09/614,912
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,401
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,412
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/146,650
 ; PRIOR FILING DATE: 1999-07-30


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; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1555
; TYPE: DNA
; ORGANISM: Zea mays
US-09-614-912-1

Alignment Scores:
Pred. No.: 3,92e-107 Length: 1555
Score: 957.50 Matches: 191
Percent Similarity: 70.75% Conservative: 46
Best Local Similarity: 57.01% Mismatches: 83
Query Match: 54.78% Indels: 15
DB: 3 Gaps: 4

US-10-670-454-2 (1-331) x US-09-614-912-1 (1-1555)

QY 1 MetValValLeuSerGln---ProAlaLeuAsnGlnPhePheLeuLeuLysProPheLys 19
DB 118 ATGGTGGTCTCGCAACCGCTGTCGTCACACAGATCCCGCTCTCTGGGTCCCGGGC 177
QY 20 SerThrProLeuPheThrGlyLeProValValAspLeuThrHisProAspAlaLysAsn 39
DB 178 CCCAGGACAGCTTCTCGGGAGTGGCGGTGCTCGACCTGCCAGCCACCGCGCGCGG 237
QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
DB 238 GCGAGCTGTCAGCCCTCGCAGCGCTTCGGGTTCCTCAAGGTCTCAACACCGCGGTGCC 297
QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
DB 298 GCGGCCACCATGGACAGGCCGAGTCCGAGGCGGTTCAGGTTCCTCGCGAGCGGCGG 357
QY 80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyPro 99
DB 358 GACAAGGACCGCGCGGGCGCGGTACCGGTTCGGGTACGGCAGCAAGCGGATCGGGTC 417
QY 100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSer 119
DB 418 AATGGCGACATGGGGTGGTTCGAGTACCTCCCTCGCGCTCGACGCCGCGTCTCTCC 477
QY 120 -----ProLysSerLeuCysIlePheArgGluAsnProHisHisPheArg 134
DB 478 GACGCTGCGCGCTGCTCCAGCGCGG-----TTCCGG 513
QY 135 AlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeu 154
DB 514 AGCGCGCTGAACGAGTACGTGCGGGCGGTGCGGAGGTGCGGCGGTGCTGTGAGGCG 573
QY 155 MetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGlu 174
DB 574 ATGGCGGAGGCGCTCGGCAATTCGGACGCGGCGCTGAGCTCCATGCTGAGCGCGCC 633
QY 175 LysSerAspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeu 194
DB 634 GGGAGCGACACAGTGTTCGCGTGAACCACTACCCGCTTCGCCGCTGAGGCGCTG 693
QY 195 AsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArg 214
DB 694 GCGTCGACGACACCGGCTTCGSCGAGCACACCGACCCGACATCATCTCCGTCTCCG 753
QY 215 SerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThr----TrpValSerVal 233
DB 754 TCCAACGGACCTCCCGGCTGAGATCGCGCTCCGCGACGCGCGAGTGGGTCTCCGTG 813
QY 234 ProProAspGlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsn 253

; Sequence 9, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-719-108-9

Alignment Scores:
Pred. No.: 7,04e-107 Length: 1008
Score: 953.00 Matches: 186
Percent Similarity: 70.12% Conservative: 44
Best Local Similarity: 56.71% Mismatches: 96
Query Match: 54.52% Indels: 2
DB: 3 Gaps: 1

US-10-670-454-2 (1-331) x US-09-719-108-9 (1-1008)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLysProPheLysSer 20
DB 1 ATGGTAATGTGTTACAGCCAGCCAGTTTGTATAGCAACTCTATGTTTAAATCCAAATGC 60
QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
DB 61 AAACCGCGTCCGGTTTAAATCCCTGTATAGACTTAACCGACTCAGATGCCAAACCCAA 120
QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
DB 121 ATCGTCAAGGCATGTGAAGAGTTTGGGTTCCTTCAAAGTCAACCATCGGGTCCGACC 180
QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
DB 181 GATCTTTGACTCAGTTGGAGCAAGGACCATCAACTTCTTTCCTTGGCATCACTCTCTC 240
QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
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; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1243, 1265)
; OTHER INFORMATION: unidentified residue
US-09-719-108-5

Alignment Scores:
Pred. No.: 1,14e-104 Length: 1318
Score: 936.50 Matches: 185
Percent Similarity: 72.16% Conservative: 56
Best Local Similarity: 55.39% Mismatches: 74
Query Match: 53.58% Indels: 19
DB: 3 Gaps: 5

US-10-670-454-2 (1-331) x US-09-719-108-5 (1-1318)
Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLyseProPheLySer 20
Db 41 ATGGCGGTATTGCTAAACCGGTA-----GCA 67
Qy 21 ThrProLeu-----PheThrGlyIleProValValAspLeuThrHisProAspAlaLyS 38
Db 68 ATACCAAAATCCGGTTCTCTCTAATCCCGGTTATAGATATGCTGACCCAGAAATCCAA 127
Qy 39 AsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLySLeuValAsnHisGlyVal 58
Db 128 CATGCCCTCGTAAAGCATCGAAGACTTCGGCTTCTTCAAGGTGATCAACCATGCGGTT 187
Qy 59 ProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLySLeuSerGln 78
Db 188 TCCGCAGAGTAGTCTCTGTTTTAGAACACGAGACCGTCGATTTCTCTCGTTGCCCAAG 247
Qy 79 SerGluLySAspArg---AlaGlyProProAspProPheGlyTyrGlySerLySArgIle 97
Db 248 TCAGAGAAAACCCAAAGTCGCAGGT-----TATCCCTTCGGATACGGACAGTAGAT 301
Qy 98 GlyProAsnGlyAspValGlyTyrValGlyTyrLeuLeuLeuAsnThrAsnProAspVal 117
Db 302 GGTCCGAATGGTGACGGTGGGTGGTTGGTTGAGTACTTGTGTGACGCTAATCATGATTC 361
Qy 118 IleSerProLySerLeuLeuPheArgGluAsnProHisPheArgAlaValVal 137
Db 362 GGTTCCGGTCCACTATTATCCAAAGTCCTCTCAAAAGCCCGGAACTTTTCAGAAACGCA 421
Qy 138 GluAsnTyrIleThrAlaValLySAsnMetCysTyrAlaValLeuGluLeuMetAlaGlu 157
Db 422 GAAGAGTACACAACATCAGTGAGAAAATGACATTCGATGTTTGGAGAAAGATCACAGAT 481
Qy 158 GlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLySAspGluLySerAsp 177
Db 482 GGGCTAGGGATCAAAACCCAGGAACACACTTAGCAAGCTTGTGTCTGACCAAAACACGG 541
Qy 178 SerCysPheArgLeuAsnHisTyrProProCysPro-----GluValGlnAlaLeu 194
Db 542 TCGATATTGAGACTTAATCACTATCCACCATGTCTCTTAGCAATAAGAAACCAATGGT 601
Qy 195 AsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArg 214
Db 602 GGTAAGAATGTGATGGTTTGGGTGAACACACACATCCTCAAAATCATCTCTGTCTTAAGA 661
Qy 215 SerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValPro 234
Db 662 TCTAACCAACACTTCTGGTCTCCAATTAATCATTAATGATGGCTCATGATCTCTGTCCCT 721
Qy 235 ProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGly 254
Db 722 CCCGATCACACTTCCTCTCTTCAACCGTTGGTGACTCTCTCCAGGTGATGACAAATGG 781
Qy 255 ArgPheLySerValLySHisArgValLeuAlaAspThrThrLySLeuSerArgLeuSerMet 274
Db 782 AGGTTCAAGACCGTGAGCATAGGGTTTTAGCTAACTGTAATAAATCTAGGGGTTCTATG 841

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RESULT 11
US-09-719-108-5
; Sequence 5, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1318
; TYPE: DNA

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Db 163 AGAATGGACGACAGTCTATAAATCTTTCTTAAACCGGCTCAGCAGAGAAATCTGTCT 222
Qy 85 GlyProProAsp---ProPheGlyTyrGlySerLysArgIleGlyProAsnGlyAspVal 103
Db 223 CGACCATTTAACCGCTTTCCGGTATGTTTATAGACATTTGGACTCAACGGTGTACTCT 282
Qy 104 GlyTTPValGluTyrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 123
Db 283 GGTGAGGTGAGTATTTGCTGTTTACACTAACGACCCCTGCC----- 324
Qy 124 CysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyrIleThrAla 143
Db 325 -----TTTCGC---FCTCAGCTCTCTTCACTCGCAGTGAATTTTACATAGAACA 375
Qy 144 ValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGln 163
Db 376 GTTAAGCAGTTGGCTCGTGAGATCTTAGATCTGACGGCTGAGGACTTCATGTC---CCA 432
Qy 164 ArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPheArgLeuAsn 183
Db 433 CCTCAGATTTTCTAGTAGTTAATACAGCTCCGTCGATAGTACTCCGTTCTGAGAGTGAAT 492
Qy 184 HisTyrProCysProGluVal-----GlnAlaLeuAsn 195
Db 493 CATTATCCACCGTCCGATCAATCTTTGTGTAAGCCCAATCTTTGACCAATCTGTGTCA 552
Qy 196 ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSer 215
Db 553 CTGACAAGAGTTGGCTTCGAGACACACACCGACCTCAGATTTTAACAGTCTTAGACT 612
Qy 216 AsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTTPValSerValProPro 235
Db 613 AACGGTGTAGGAGGGTCCCAAGTGTCCATTCAGATGGCATGTGGGTTTCTGTCTCCCT 672
Qy 236 AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg 255
Db 673 GACCTTTCAGCTTTCTGCGTCAATGTAGGAGACTTGTACAGGTGATGACGAACGGGAGA 732
Qy 256 PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle 275
Db 733 TTTATAAGTGTAAAGCATAGACATTTGACTACGGAGAGAAAGCGGCTATCCACGGCG 792
Qy 276 TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSer---ValMetLeu 294
Db 793 TACTTTGCGGACCAACCGCTTCAGGCGAAGATTGGGCTCTTTCGCGCATGTTATGACG 852
Qy 295 LysGlyGluGluCysLeuTyrLysGluPheThrTTPCysGluTyrLysAlaAlaTyr 314
Db 853 ATGAATCAGCCACGGTTGTACCAACATTTACTTGGGGCGGATACAAAGAACTTGGGTAC 912
Qy 315 ThrSerArgLeuAlaAspAsnArgLeuAlaProPheGln 327
Db 913 TCTCTACGACTTGAGNTAGCGTTTAGACATGTTTCGT 951
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RESULT 14

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US-09-371-307-71
; Sequence 71, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Pilller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 811
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-307-71

Alignment Scores:
Pred. No.: 6,14e-58 Length: 811
Score: 553.00 Matches: 108
Percent Similarity: 71.88% Conservative: 30
Best Local Similarity: 56.25% Mismatches: 48
Query Match: 31.64% Indels: 6
DB: 3 Gaps: 2

US-10-670-454-2 (1-331) x US-09-371-307-71 (1-811)
Qy 140 TyrIleThrAlaValLysAsnMetCysTyrAlaValAlaValLeuGluLeuMetAlaGluGlyLeu 159
Db 2 TACACGGTGGCGGTGCGCGGATGCGTGGCGGCTGGTGGCGGCTGATGGCGAGGGGCTG 61
Qy 160 GlyIle-----ArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSer 176
Db 62 GGCATCGCGCGCGCGCGGACCGCGTGTGGCGCGGCTGGTGGCGCGGACGAC 121
Qy 177 AspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArg 196
Db 122 GACTGCATGCTCGGGTGAACCACTATCCCGCGCGCGCG-----GCGCTCAACCCC 172
Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSer 216
Db 173 AGCCTCAGCGGGTTCGGCGGACACACCGACCGCAGATCATCTCGGTGCTCCGCGCCAC 232
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTTPValSerValProProAsp 236
Db 233 GGCACCTCGCGCTGGAGATCGCGTGGCGGACCGCGCTGGGCTCGTCCGCGCCGAC 292
Qy 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 293 GGGGACGCTTCTTCGTCAACGTCGCGACACCCCTGCAAGTGTTCGCAACCGGAGGTTTC 352
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
Db 353 AGGAGCGTGGAGCAGCGGTGTGGTGAACGCGAGAAAGTCCCGGTGTCCATGCTCTTC 412
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db 413 TTCGCGCGCGCGCGCGCGGAGGCTGGGCGCGCTTCGCGACGCTCTTGGCGGACGCGC 472
Qy 297 GluGluCysLeuTyrLysGluPheThrTTPCysGluTyrLysAlaAlaTyrThrSer 316
Db 473 GCGCGGAGCGGTACCGGGACTTCACCTGGAGCGAGTTCAGACCCAGCGGGGTGCAGGACC 532
Qy 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 533 AGGCTCGCGAAGACCGGCTGTCCGCTTCGAGAG 568
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RESULT 15

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US-09-371-307-68
; Sequence 68, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Pilller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
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; CURRENT APPLICATION NUMBER: US/09/371,307A
 ; CURRENT FILING DATE: 1999-08-10
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 68
 ; LENGTH: 406
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (306)
 ; OTHER INFORMATION: n = a, c, g, or t
 US-09-371-307-68

Alignment Scores:
 Pred. No.: 7.5e-45 Length: 406
 Score: 442.50 Matches: 87
 Percent Similarity: 75.71% Conservative: 19
 Best Local Similarity: 62.14% Mismatches: 25
 Query Match: 25.31% Indels: 9
 DB: 3 Gaps: 4

US-10-670-454-2 (1-331) x US-09-371-307-68 (1-406)

QY	83	ArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsnGlyAsp	102
DB	2	AAACAGGACAAACCCAGCCTTATGCTATGTAATAAAGGATTGGACCAATGGTGAT	61
QY	103	ValGlyTyrPValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerProLysSer	122
DB	62	GTTGGTGGGTGGATATCTCTCTCCACCAACCAAGAC-----CCGAATCTC	112
QY	123	LeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyrIleThr	142
DB	113	CTT-----GGAACCTGAAACCCAGAGAGTTTCAGGATTGCTTTGGATAATTATATGGCA	166
QY	143	AlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArg	162
DB	167	GCAATGAGAAATGGCATCTGAGATACTTGAATGATAGCTGATGGGCTAAGGTTTCAG	226
QY	163	GlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPheArgLeu	182
DB	227	CCAAGAAATGTGTTAAGTAAGCTGATGATGATGAACAGAGTGACTCTGTTTTCAGGCTG	286
QY	183	AsnHisTyrProProCysProGlu---ValGlnAlaLeuAsn-----ArgAsnLeu	198
DB	287	AACCATACCCCTCCGTCNAGAGGTGGTTCAGTCTTGAATGGAAACGAGCAGTAATGTG	346
QY	199	ValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThr	218
DB	347	ATTGGATTGGTGAAACACACTGACCCACAAATCATTTTCAGTCTTAAGATCCACACACT	406

Search completed: December 28, 2005, 04:48:40
 Job time : 256 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2005, 01:30:23 ; Search time 975 Seconds

(without alignments)
2807.348 Million cell updates/sec

Title: US-10-670-454-2

Perfect score: 1748

Sequence: 1 MVVLSQPALNQFLLKPKFS.....AAYTSRLADNLAPQKSA 331

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA Main.*

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9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*

10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1748	100.0	999	8	US-10-821-711-3
2	1748	100.0	1318	8	US-10-670-454-1
3	1530.5	87.6	1359	3	US-09-371-307-62
4	1530.5	87.6	1359	6	US-10-401-321-62
5	1092.5	62.5	1026	3	US-09-938-842A-1350
6	1092.5	62.5	1026	3	US-09-938-842A-1350
7	1092.5	62.5	1237	8	US-10-670-454-7

Alignment Scores:

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Score: 1748.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 8
Length: 999
Matches: 331
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

ALIGNMENTS

RESULT 1

US-10-821-711-3

; Sequence 3, Application US/10821711

; Publication No. US20040237142A1

; GENERAL INFORMATION:

; APPLICANT: Gilbertson, Larry A

; APPLICANT: Krieger, Elysia K

; APPLICANT: Ye, Xudong

; APPLICANT: Zhang, Wanggen

; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF

; FILE REFERENCE: 38-21(52967)B

; CURRENT APPLICATION NUMBER: US/10/821,711

; PRIOR FILING DATE: 2004-04-08

; PRIOR APPLICATION NUMBER: 60/461,459

; NUMBER OF SEQ ID NOS: 16

; SEQ ID NO 3

; LENGTH: 999

; TYPE: DNA

; ORGANISM: Phaseolus coccineus

US-10-821-711-3

Sequence 64, Appl
Sequence 64, Appl
Sequence 21951, A
Sequence 3, Appl1
Sequence 78659, A
Sequence 69575, A
Sequence 9, Appl1
Sequence 141, Appl
Sequence 5, Appl1
Sequence 1288, Ap
Sequence 4257, Ap
Sequence 103352,
Sequence 67, Appl
Sequence 67, Appl
Sequence 1, Appl1
Sequence 16086, A
Sequence 6183, Ap
Sequence 129307,
Sequence 7861, Ap
Sequence 58, Appl
Sequence 58, Appl
Sequence 177171,
Sequence 159585,
Sequence 34429, A
Sequence 71, Appl
Sequence 20123, A
Sequence 614, App
Sequence 9278, Ap
Sequence 82089, A
Sequence 68, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 136729,
Sequence 66, Appl
Sequence 66, Appl

US-10-670-454-2 (1-331) x US-10-821-711-3 (1-999)

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Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db 1 ATGGTTGTTCTGTCTCAGGCAGCATTTGAACAGTCTTCTCTGAAACCATTTCAAGTCC 60
Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 61 ACGCCCTTGTTCACGGGGATTCCTGTGTGCAGCTCAGCACCCCGATGCCAAGATCTC 120
Qy 41 IleValAsnAlaCysArgAspPheGlyPheLeuValAsnHisGlyValProLeu 60
Db 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATTG 180
Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysSerGlnSerGlu 80
Db 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
Qy 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 241 AAAGACAGAGCTGTGTCCTCCCGACCTTCGGCTATGGTAGCAAGAGGATGGCCCAAC 300
Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 301 GGTGATGTGGTGGTTCGAATACCTCTCTCAACACCAACCTCGATGTATCTCACCC 360
Qy 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 361 AAATCACTTTGCAATTTCCGAGAAAATCCTCATCTTTCAGGGCGGTGGTGAGAACTAC 420
Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 421 ATTACAGCAGTGAAGAACATGCTGCTATGCGTGTGGATTTGATGCGGAGGGGTGGG 480
Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 481 ATAAGGCAGAGGAATACGTTAAGCAGGTTCGTAAGGATGAGAAAAGTGAATCGTGCTTC 540
Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
Db 541 AGGTTGAACCACTACCCGCTTCCTCCGAGTGCAGCACTGAACCGGAATTTGGTGGG 600
Qy 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnThrSerGly 220
Db 601 TTTGGGAGACACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC 660
Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
Db 661 TTGCAAAATCTGTCTCAGATGGCACTTGGGTTTTCAGTCCACCTCGATCAGACTTCCTTT 720
Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 721 TTCATCAATGTGGTCAGCTCTACAGGTAAATGACTAATGGGAGGTTTAAAGTGTAAAG 780
Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 781 CATAGGTTTTGGCTGACACAGAGTCAAGGTATCAATGATCTACTTTGGAGACCA 840
Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
Db 841 GCGTTGAGTGAAATAATAGCACCTTTTACCTTCAGTGATGTTAAAGGAGAGGAGTGTGTG 900
Qy 301 TyrLysGluPheThrTrpCysGluTyrLysLeuAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 901 TACAAAAGAGTTTCATGGTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 961 AATAGGCTTCCCTTTCCAGAAAATCTGCTGCT 993

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RESULT 2

US-10-670-454-1

; Sequence 1, Application US/10670454

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; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-10-670-454-1

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Alignment Scores:

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Pred. No.: 3,55e-219 Length: 1318
Score: 1748.00 Matches: 331
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

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US-10-670-454-2 (1-331) x US-10-670-454-1 (1-1318)

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Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db 68 ATGGTTGTTCTGTCTCAGGCAGCATTTGAACAGTCTTCTCTGAAACCATTTCAAGTCC 127
Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 128 ACGCCCTTCTTTCAGCGGGATTCCTGTGTGTGCAGCTCAGCACCCCGATGCCAAGATCTC 187
Qy 41 IleValAsnAlaCysArgAspPheGlyPheLeuValAsnHisGlyValProLeu 60
Db 188 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 247
Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 248 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
Qy 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 308 AAAGACAGAGCTGTGTCCTCCCGACCTTCGGCTATGGTAGCAAGAGGATGGCCCAAC 367
Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 368 GGTGATGTGGTGGTTCGAATACCTCTCTCAACACCAACCTCGATGTATCTCACCC 427
Qy 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 428 AAATCACTTTGCAATTTTCGAGAAAATCCTCATCTTTCAGGGCGGTGGTGAGAACTAC 487
Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 488 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTCGAAATGATGCGGAGGGGTGGG 547
Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 548 ATAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATCTGCTGCTTC 607
Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200

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Db 608 AGTTGAACCACTACCCGCTTGCCTGAGGTGCGACACTGAACCGGAATTTGTTGGG 667
 Qy 201 PheGlyGluHisThrAspProGlnIleSerValLeuArgSerAsnSerThrSerGly 220
 Db 668 TTTGGGAGCACACAGACCCACAGATAATTTCTGCTCTTAAGACTTAACAGCACATCTGGC 727
 Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 240
 Db 728 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCACACCTGATCAGACTTCCTTT 787
 Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLeuSerVallys 260
 Db 788 TTCATCAATGTTGGTGACGCTCTACAGGTAAATGACTAATGGAGGTTTTAAAGGTGAAG 847
 Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
 Db 848 CATAGGGTTTTGGCTGACACAAAGTCAAGTTATCAATGATCTACTTTGGAGGACCA 907
 Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysLeu 300
 Db 908 GCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGTATTTAAAGAGGAGAGTGTGTTG 967
 Qy 301 TyrLysGluPheThrTrpCysGluTyrLysValAlaTyrThrSerArgLeuAlaasp 320
 Db 968 TACAAGAGTTTCACATGTTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
 Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
 Db 1028 AATAGGCTTGCCCTTTCCAGAAATCTGCTGCT 1060

RESULT 3

US-09-371-307-62
 ; Sequence 62, Application US/09371307A
 ; Patent No. US20020053095A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Sherri M.
 ; APPLICANT: Heck, Gregory R.
 ; APPLICANT: Pillier, Kenneth J.
 ; APPLICANT: Kishore, Ganesh M.
 ; APPLICANT: Ellich, Tedd D.
 ; APPLICANT: Logusch, Eugene W.
 ; APPLICANT: Rao, Sudabathula
 ; APPLICANT: Ream, Joel E.
 ; APPLICANT: Logusch, Sherry J.
 ; TITLE OF INVENTION: Methods for controlling gibberellin levels
 ; FILE REFERENCE: MOST:216
 ; CURRENT APPLICATION NUMBER: US/09/371,307A
 ; CURRENT FILING DATE: 1999-08-10
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 62
 ; LENGTH: 1359
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-09-371-307-62

Alignment Scores:
 Pred. No.: 1,78e-190 Length: 1359
 Score: 1530.50 Matches: 296
 Percent Similarity: 90.36% Conservative: 4
 Best Local Similarity: 89.16% Mismatches: 31
 Query Match: 87.56% Indels: 1
 DB: 3 Gaps: 1

US-10-670-454-2 (1-331) x US-09-371-307-62 (1-1359)

Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
 Db 102 ATGGTGTGTTCTCTCAGCCAGCATTAACCAAGTTTCTCTCTGAAACATGCAAGCC 161
 Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 Db 162 ACGCCCTTGTTCGGGGGATTCTCTGTGGTGCACCTTCAGGACCCCGCATGCCAAGACCCAC 221

Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 Db 222 ATAGTCAATGCTCAGGACCTTCGGCTTCTTCAAGCTCGTGAACCAACCGGTTCCGTTA 281
 Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
 Db 282 CAGTTCATGGCCAAATTTGGAAACGAAACCTTCGGGTCTTCAAAAACCTCAATCCGAG 341
 Qy 81 LysAspArgAlaGlyProProAspPheGlyTyrGlySerLysArgIleGlyProAsn 100
 Db 342 AAAGACAGGGCTGTCTCCCTGACCTTTGGCTACGGCAGCAAGAGGATTTGGCCCTAAC 401
 Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuAsnThrAsnProAspValIleSerPro 120
 Db 402 GCGCATGTGGTGGTTCGAATACCTCTCTCAACCAACCAACCTGTATGTCTATCTCCCCC 461
 Qy 121 LysSerLeuCysIlePheArgGluAsnProHishi sPheArgAlaValValGluAsnTyr 140
 Db 462 AAGTCACAGTTTCATTTTCAGAGAAGGCTCTCAGAAATTTTCAGGGCGGTGGTGAGGAATAC 521
 Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
 Db 522 ATTAGCGGGTGAAGACATGTGCTATGAGGTGTTGGAATTTGATGGCTGAGGGATTGGG 581
 Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerSerSerCysPhe 180
 Db 582 ATAACGCGCAGAGGAATGTGTTGAGTAGTGTGTAAGGATGAGAAGAGTGATYCTTGTCTC 641
 Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn--ArgAsnLeuVal 199
 Db 642 AGACTTAACCACTACCCGCCATGCCGAGGTGCAAGCATTTGAACGGGAAGAAATTTGGTT 701
 Qy 200 GlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSer 219
 Db 702 GGATTTGGAGGACACACAGACCCACAGATAATTTCTGCTTTGAGATCTTAACGACCTCA 761
 Qy 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSer 239
 Db 762 GGCCTTGCAAAATCTGCTCACAGATGGCATTGGGTTCTGTCCTCCACCTGATCAAACTTCC 821
 Qy 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
 Db 822 TTTTTCATCATGTTGTTGGTGCACACTCTTCAGGTAAATGACTAATGGAGGTTTTAAAAGTGT 881
 Qy 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
 Db 882 AAGCATAGAGTTTGGCTGACCCCAACCAAGTCAAGTTGTCAATGATCTACTTTTGGAGGA 941
 Qy 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
 Db 942 CCACCTTGTGTGAAAGATAGCACCTTTACCTTCACTCATGTTTAAAGAGGAGAGAGT 1001
 Qy 300 LeuTyrLysGluPheThrTrpCysGluTyrLysValAlaTyrThrSerArgLeuAla 319
 Db 1002 TTCTACAAAGAGTTTCACATGTTGGGAAATACAAAGGCTGCGTACGCGTCAAGGCTAGCG 1061
 Qy 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
 Db 1062 GATAATAGACTCGGCCCTTTTGGAGAAATCTGCTGCT 1097
 RESULT 4
 US-10-401-321-62
 ; Sequence 62, Application US/10401321
 ; Publication No. US20030233679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Sherri M.
 ; APPLICANT: Heck, Gregory R.
 ; APPLICANT: Pillier, Kenneth J.
 ; APPLICANT: Kishore, Ganesh M.
 ; APPLICANT: Ellich, Tedd D.
 ; APPLICANT: Logusch, Eugene W.
 ; APPLICANT: Rao, Sudabathula

APPLICANT: Ream, Joel E.
APPLICANT: Logusch, Sherry J.
APPLICANT: Baerson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REFERENCE: 11899.0216.DVUS01 (MOBT-216--1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 1359
TYPE: DNA
ORGANISM: Glycine max
US-10-401-321-62

Alignment Scores:
Pred. No.: 1.78e-190 Length: 1359
Score: 1530.50 Matches: 296
Percent Similarity: 90.36% Conservative: 4
Best Local Similarity: 89.16% Mismatches: 31
Query Match: 87.56% Indels: 1
DB: 6 Gaps: 1

US-10-670-454-2 (1-331) x US-10-401-321-62 (1-1359)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db 102 ATGGTTGTTCTCTCAGCAGCATTAACACGATTTTCTCTGAAACATGCAAGCCC 161
QY 21 ThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 162 AGCCCTTGTTCGCGGGATTCGTGTGTCGACCTCAGGACCCCGATGCCAAGACCCAC 221
QY 41 IleValAsnAlaCysArgAspPheGlyPheLeuValAsnHisGlyValProLeu 60
Db 222 ATAGTCAATGCCCTGCAGGACATTCGGCTCTTCAAGCTGTGAACACACCGTGTTCGTTA 281
QY 61 GlyMetMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 282 CAGTTCATGCCAATTTGGAAACGAAACCTCGGGTCTTCAAAAACCTCAATCCGAG 341
QY 81 LysAspArgAlaGlyProAspPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 342 AAAGACAGGCTGTCCTCCCTGACCTTTGGTACGGCAGCAAGAGGATTGGCCCTAAC 401
QY 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 402 GCGATGTTCGGTGGGTGGAATACCTCTCAACACCAACCCCTGATGTCATCTCCCCC 461
QY 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 462 AGTCAAGTTCATTTTCAGAGAGTCTCTCAGAAATTCAGGCGGTGTGGAGGAATAC 521
QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 522 ATTAGACGCTGAAGAACATGTCTATGAGGTGTGGAATTCATGCTGAGGATTTGGG 581
QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 582 ATAACCCAGAGGAATGTGTGATGATGCTGGAAGGATGGAAGAGTGTATCTTGCCTTC 641
QY 181 ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsn--ArgAsnLeuVal 199
Db 642 AGACTTAACCATACCCCGCATCCCGAGGTGCAAGCATTTGAACGAAGGAATTTGGTT 701
QY 200 GlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSer 219
Db 702 GGATTTGGAGAGACACACAGACCCACAGATAATTTCTGTCTTGAGATCTTAACAGCACCTCA 761
QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSer 239
Db 762 GGCCTGCAAACTGTCTCAGATGGCACTTGGGTTTCTGTGCCACCTGATCAAACTTCC 821

QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
Db 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTAATGCGAGGTTTAAAGTGTA 881
QY 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
Db 882 AAGCATAGAGTTTGGCTGACCCAAAGTCAAGGTTGTCAATGATCTACTTTTGAGGA 941
QY 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlyCys 299
Db 942 CCACCTTGTGTGAAAAGATAGCACCTTTTACCTTCACTCATGTTTAAAGGAGAGAGT 1001
QY 300 LeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAla 319
Db 1002 TTCTACAAAGAGTTTCACATGGTGGGAATACAAGAGGCTGGTACGCTCAAGGCTAGCG 1061
QY 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097
RESULT 5
US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1350
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350
Alignment Scores:
Pred. No.: 6.49e-133 Length: 1026
Score: 1092.50 Matches: 210
Percent Similarity: 76.81% Conservative: 45
Best Local Similarity: 63.25% Mismatches: 72
Query Match: 62.50% Indels: 5
DB: 3 Gaps: 3
US-10-670-454-2 (1-331) x US-09-938-842A-1350 (1-1026)
QY 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
Db 1 ATGGTGGTTCGTCACAGCCAGTCATCTTAGATTAACCATCTCCCTAATCCCCACATAC 60
QY 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
Db 61 AAACCGGTTCCGGTTCCTCCTCCCATTCATTCCTCCGTCGTCACCTAGCCGATCCGGAA 120
QY 37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHis 56
Db 121 GCGAAACCCGAATCGTAAAGCCCTGCGAGGAGTTCCGGTTCCTTCAAGGTCGTAACAC 180
QY 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLys 76
Db 181 GGAGTCCGACCCGAATCATGCTCGTTAGACGAGGAGGCTATTGGCTTCTTCTCGGCTTG 240


```
Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspPropheGlyTyrGlySerLysArg 96
Db 241 CCTCAGTCTCTTAAACACCGGCGGTCCACCTGAACCGGTACGGTTATGTTAAACCGG 300
Qy 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuAsnThrAsnProAsp 116
Db 301 ATTGGACCAACACCGGTGAGTGGTTGGATTGAGTATCTCCCTCAATGCTTAATCCTCAG 360
Qy 117 ValIleSerProLysSerLeuCysIlePheArgGlnAsnProHisPheArgAlaVal 136
Db 361 CTCCTCTCTCTTAAACCTCCCGCTTTCGGTCAACCCCTCAAAATTTTCGGTGAGTCG 420
Qy 137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla 156
Db 421 GTGAGGAGTACATGAAGGAGTAAAGGAGTGTCTGTAACAAGTGTTCGAGATGTTGCC 480
Qy 157 GluGlyLeuGlyIleArgGlnAsnThrLeuSerArgLeuLeuLysAspGlySer 176
Db 481 GAAGAACTAGGGATAGACCCAGGACACTCTGAGTAAATGCTGAGAGTGAAGAAGT 540
Qy 177 AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196
Db 541 GACTCGTCCCTGAGACTAAACCATTTATCCGGCGCGGAGGAA--GAGCGGAGAGATG 597
Qy 197 AsnLeuValGlyPheGlyHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db 598 GTGAAGGTGGGGTTTGGGGAACACACAGACCACAGATAATCTCAGTCTAAGATCTAAT 657
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAsp 236
Db 658 AACACGGGGTCTTCAAAATCTGTGAAAGATGGAAGTGGGTGCTGCTCCCTCTGAT 717
Qy 237 GlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 718 CACTCTCTCTTCAATTAATGTTGAGATGCTCTCAGGTATGAGTTATGACTAACGGAGGTC 777
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
Db 778 AAGAGTGTAAACACAGGGTCTTAGCCGATACAAGGAGATCGAGGATTTCAATGATATAT 837
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db 838 TTCGGCGGACCGCCATTGAGCCAGAGATCGCACCAATTTGCCATTTGCTCCCTGAGCAA 897
Qy 297 GluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSer 316
Db 898 GATGATGGCTTTTCAAAAGAAATTCATCTGCTCAATACAAATCTTCTGTACAGTCT 957
Qy 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 958 AAGCTTGGTGATTATAGACTTGGTCTCTTTGAGAA 993
RESULT 6
US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
```

```
; SEQ ID NO 1350
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350
Alignment Scores:
Pred. NO.: 6,49e-133 Length: 1026
Score: 1092.50 Matches: 210
Percent Similarity: 76.81% Conservative: 45
Best Local Similarity: 63.25% Mismatches: 72
Query Match: 62.50% Indels: 5
Db: 3 Gaps: 3
US-10-670-454-2 (1-331) x US-09-938-842A-1350 (1-1026)
Qy 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
Db 1 ATGTGTGGTTTGGCCACAGCCAGTCACCTTTAGATACACCATCTCTCCCTAATCCCCACATAC 60
Qy 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
Db 61 AAACCGGTTCCGGTTCTCCTCCATTCATCCCGTCGTCAACCTAGCCGATCCGAA 120
Qy 37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis 56
Db 121 GCGAAACCCGAAATCGTAAAGCCCTGCGAGGAGTTCGGGTCTTCAAGGTCTGTAACCCAC 180
Qy 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys 76
Db 181 GGAGTCCGACCCGAACTCATGACTCGGTAGACGAGGAGGTATTTGGCTTCTTCGGCTTG 240
Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspPropheGlyTyrGlySerLysArg 96
Db 241 CCTCAGTCTCTTAAACACCGGCGGTCCACCTGAACCGGTATGTTAAATAACCGG 300
Qy 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuAsnThrAsnProAsp 116
Db 301 ATTGGACCAACACCGGTGAGTGGTTGGATTGAGTATCTCTCTCAATGCTTAATCCTCAG 360
Qy 117 ValIleSerProLysSerLeuCysIlePheArgGlnAsnProHisPheArgAlaVal 136
Db 361 CTCCTCTCTCTTAAACCTCCCGCTTTCGGTCAACCCCTCAAAATTTTCGGTGAGTCG 420
Qy 137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla 156
Db 421 GTGAGGAGTACATGAAGGAGTAAAGGAGTGTCTGTAACAAGTGTTCGAGATGTTGCC 480
Qy 157 GluGlyLeuGlyIleArgGlnAsnThrLeuSerArgLeuLeuLysAspGlySer 176
Db 481 GAAGAACTAGGGATAGACCCAGGACACTCTGAGTAAATGCTGAGAGATGAGAAGAGT 540
Qy 177 AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196
Db 541 GACTCGTCCCTGAGACTAAACCATTTATCCGGCGCGGAGGAA--GAGCGGAGAGATG 597
Qy 197 AsnLeuValGlyPheGlyHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db 598 GTGAAGGTGGGGTTTGGGGAACACACAGACCACAGATAATCTCAGTCTAAGATCTAAT 657
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAsp 236
Db 658 AACACGGGGTCTTCAAAATCTGTGAAAGATGGAAGTGGGTGCTGCTCCCTCTGAT 717
Qy 237 GlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 718 CACTCTCTCTTCAATTAATGTTGAGATGCTCTCAGGTATGAGTTATGACTAACGGAGGTC 777
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
Db 778 AAGAGTGTAAACACAGGGTCTTAGCCGATACAAGGAGATCGAGGATTTCAATGATATAT 837
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
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Percent Similarity: 76.44% Conservative: 53
Best Local Similarity: 60.42% Mismatches: 72
Query Match: 60.64% Indels: 6
DB: 3 Gaps: 3

US-10-670-454-2 (1-331) x US-09-371-307-64 (1-1403)

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Qy 1 MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer 20
Db 149 ATGGTGTGCTCTCAAGGCAACAAAGCAACAACTACTCTACATCAAGAACTACATGCCA 208
Qy 21 ThrProLeuPheThrGlyIleProValValAlaLeuThrHisProAspAlaLysAsnLeu 40
Db 209 ACGCATTCCTCCTCAACAATTCCTGAGGACCTCTCCAAACACAGATGCAAGACCCCTC 268
Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 269 ATAGTGAAGGCTGTGTGAGGAATTTGGATTCTTCAAAAGTCATCAACCATGTTGCCATG 328
Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 329 GAAACTATATCCCAATTCGAATCTGAAGCTTCAAGTTCTTCTCTATGCCACTCAATGAG 388
Qy 81 LysAspArgAlaGlyProProAspPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 389 AAGGAAAAGTAGGCCCTCCCAACCATATGGTATGGTATGGTATGGTATGGTATGGTATG 448
Qy 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
Db 449 GGGGATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 496
Qy 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 497 CACAATTCCTCTGTTTATGGCAAAACCGCTGAGAAATTTAGGTGTTTGTGTAACCATG 556
Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 557 ATGCTCTCTGAGGAAATGGCATGTGAGATTTCTTCAAAAGTCATCAACCATGTTGCCATG 616
Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspCysPhe 180
Db 617 ATACAAACAAAATATGTTTATGAGGCTTCTTATGGATATGAGATGAGATGAGATGAG 676
Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
Db 677 AGGTGATCATCATCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733
Qy 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
Db 734 TTTGAGAAACACACGAGCCCAACAATCATTTCTTACTTAGTTCACCAATACCTTTCAGGC 793
Qy 221 LeuGlnIleCysLeuThrAspGlyThrTyrValSerValProProAspGlnThrSerPhe 240
Db 794 CTTTCAGATTTTCTTAGAGATGGAACTGAGATTTTCAAGTCCCACTGATCACAATACTTTC 853
Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 854 TTCATAATGTTGGTATGTTCTTTCAGGTATGACCAATGAGAGTTTTCGAGTGTGAAA 913
Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 914 CACAGATTTTTCACAAATGGAATTAAGTCTAGCTACTCTCAATGATTTACTTTTGGAGG 973
Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysLeu 300
Db 974 CCAATTTGAGTGAAAATATGATACCATTTATCTTCACTTATG---AAAGGAAAAGAAAGCTTA 1030
Qy 301 TyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 1031 TACAAAGAGTTTACGTGGTTCGAGTATATAAATTTAACTATGCTTCAAGATGCTGCTGAT 1090
Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
```

Db 1091 AATAGGCTTGACATTTTGGAGAAATGTTGCT 1123

RESULT 9

US-10-401-321-64

; Sequence 64, Application US/10401321

; Publication No. US20030233679A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Sherri M.

; APPLICANT: Heck, Gregory R.

; APPLICANT: Piller, Kenneth J.

; APPLICANT: Kilshore, Ganesh M.

; APPLICANT: Ellich, Ted D.

; APPLICANT: Logusch, Eugene W.

; APPLICANT: Rao, Sudabathula

; APPLICANT: Ream, Joel E.

; APPLICANT: Logusch, Sherry J.

; APPLICANT: Baerson, Scott R.

; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels

; FILE REFERENCE: 11899-0216.DVUS01 (MOBT:216--1)

; CURRENT APPLICATION NUMBER: US/10/401.321

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 64

; LENGTH: 1403

; TYPE: DNA

; ORGANISM: Glycine max

US-10-401-321-64

Alignment Scores:

Pred. No.: 2,06e-128 Length: 1403

Score: 1060.00 Matches: 200

Percent Similarity: 76.44% Conservative: 53

Best Local Similarity: 60.42% Mismatches: 72

Query Match: 60.64% Indels: 6

DB: 6 Gaps: 3

US-10-670-454-2 (1-331) x US-10-401-321-64 (1-1403)

Qy 1 MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer 20

Db 149 ATGGTGTGCTCTCAAGGCAACAAAGCAACAACTACTCTACATCAAGAACTACATGCCA 208

Qy 21 ThrProLeuPheThrGlyIleProValValAlaLeuThrHisProAspAlaLysAsnLeu 40

Db 209 ACGCATTCCTCCTCAACAATTCCTGAGGACCTCTCCAAACACAGATGCAAGACCCCTC 268

Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60

Db 269 ATAGTGAAGGCTGTGTGAGGAATTTGGATTCTTCAAAAGTCATCAACCATGTTGCCATG 328

Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80

Db 329 GAAACTATATCCCAATTCGAATCTGAAGCCTTCAAGTTCTTCTCTATGCCACTCAATGAG 388

Qy 81 LysAspArgAlaGlyProProAspPheGlyTyrGlySerLysArgIleGlyProAsn 100

Db 389 AAGGAAAAGTAGGCCCTCCCAACCATATGGTATGGTATGGTATGGTATGGTATGGTATG 448

Qy 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120

Db 449 GGGGATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 496

Qy 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140

Db 497 CACAATTCCTCTGTTTATGGCAAAACCGCTGAGAAATTTAGGTGTTTGTGTAACCATG 556

Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160

Db 557 ATGCTCTCTGAGGAAATGGCATGTGAGATTTCTTCAAAAGTCATCAACCATGTTGCCATG 616

Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspCysPhe 180


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Db 617 ATACACAAAAAATGTGTTTAGCAAGCTTCTTATAGGATAAAGAGAGTGAAGTCTCTGTTTT 676
Qy 181 ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
Db 677 AGGGTGAATCACTACCTGCTGGCTGAACCT--GTGAATGGTCAAAACATGATAGGG 733
Qy 201 PheGlyGluHisThrAspProGlnIleSerValLeuArgSerAsnSerThrSerGly 220
Db 734 TTTGGAGAACACACGAGCCACAAATCAATTTCTCTACTTAGGTCCAAACAATACTTTCAGGC 793
Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
Db 794 CTTTCAGATTTTCTTAGAGATGGAACCTGGATTTTCTAGTCCCACTGATCACAATCTTTTC 853
Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 854 TTCATTAATGTTGGTGATTTCTCTTAGGTATAGCAATGGAAGTTTCGAAGTGTGAA 913
Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 914 CACAGAGTTTGCACAAATGGATTTAAGTCTAGACTCTCAATGATTTACTTTGGAGGTCCA 973
Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysLeu 300
Db 974 CCATTGAGTGAAGAAATAGTACCATTTATCTTCACCTATG--AAAGGAAAGAAAGCTTA 1030
Qy 301 TyrLysGluPheThrTrpCysGluTyrLysAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 1031 TACAAAGAGTTTACGTGGTTCAGGTATATAAAATTTAACTTAAGTCTCAAGATTGCTGAT 1090
Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 1091 AATAGCTTGGACATTTTTCAGAGAAATTTGTGCT 1123

RESULT 10
US-10-424-599-21951
; Sequence 21951, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 21951
; LENGTH: 1390
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_119826C.1
US-10-424-599-21951

Alignment Scores:
Pred. No.: 6,17e-118 Length: 1390
Score: 980.50 Matches: 195
Percent Similarity: 75.68% Conservative: 57
Best Local Similarity: 58.56% Mismatches: 74
Query Match: 56.09% Indels: 7
DB: 7 Gaps: 3

US-10-670-454-2 (1-331) x US-10-424-599-21951 (1-1390)

Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLysProPheLysSer 20
Db 175 ATGGTGTTGCTGTCACAAACACACAGAACAAATACTCTCATCATCAGAACTACATGCCA 234
Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 211 ATGGTGTTGCTGTCACAAACACACAGAACAAATACTCTCATCATCAGAACTACATGCCA 234
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Db 235 ACTGCATTTCTCTCCAAACAATTCCTCCATAGTGGACCTCTCCAAACCTGATGCAAGACCCTT 294
Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 295 ATAGTGAAGGCTTGTGAGGAGTTTGATTTCTTCAAGTCATCAACCATGGTGTGCCCATTT 354
Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArg-PhePheLysLysSerGlnSerGly 80
Db 355 GAAAGCTATATCCCAATTCGAATATGAAGCCTTCCAAACTTCTCTCTATGCCACTCAATGA 414
Qy 80 uLysAspArgAlaGlyProProAspPheGlyTyrGlySerLysArgIleGlyProAs 100
Db 415 GAAA--AAAGTAGACCTCCCAATTCCTTGGGTGTAGCAAGAAATTCAGGTGTCTGTTGAACAGTT 471
Qy 100 nGlyAspValGlyTrpValGluTyrLeuLeuAsnThrAsnProAspValIleSerPr 120
Db 472 TGGGACGTTGGTGGATGGAGTACTCTTCTTCAACACCAAGCAA-----TCAAG 522
Qy 120 oLysSerLeu-CysIlePheArgGluAsnProHisPheArgAlaValValGluAsn 140
Db 523 AACACAACCTCTCTCTGTTATGGCAAAAACGCTGAGAAATTCAGGTGTCTGTTGAACAGTT 582
Qy 140 yrIleThrAlaValLysAsnMetCysTyrAlaValLeuLeuLeuMetAlaGlyLeuG 160
Db 583 ACATGCTTCTGTGTAGGGAAGATGGCATGTGAGATTTCTTGGTTGATGGCAGAGGGTTGA 642
Qy 160 lyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysP 180
Db 643 AGATTACGAAAGAGATGTTTAGCAAGCTTCTAATGGATAAACAAGTGAATCTTATTT 702
Qy 180 heArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValG 200
Db 703 TCAGGCTGAATCATTTACGCTGCTCTCTGAAATGACTCTGAAATGATCATCAGAACTTGATTTG 762
Qy 200 lyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerG 220
Db 763 GGTGTTGGAGAACACACAGACCCCAAAATCATCTCTGTTAAGATCCCAACACACTTCAG 822
Qy 220 lyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerP 240
Db 823 GCCTTCAGATTTATCTTAGAGATGGAATTTGATTTCCAGTCCACACAGCTCCAGCGCTT 882
Qy 240 hePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 260
Db 883 TTTTATTAACTGTTGATTTCTCTAGGTTATGACAAATGCAAGGTTCCGAAGTGTGA 942
Qy 260 ysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyP 280
Db 943 GACACAGAGTGTGGCAAAATGGGTTTCAAGTCCAGGCTTTCATGATTTACTTTGGAGGTC 1002
Qy 280 roAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysL 300
Db 1003 CACCTTTGAGTGAGAAAATAGCACCATTATCTCTCTCATG--AAAGGAAAGAAAGTTC 1059
Qy 300 euTyrLysGluPheThrTrpCysGluTyrLysAlaAlaTyrThrSerArgLeuAlaA 320
Db 1060 TATATAAAGAGTTTACCTGGTTTGGATACAAAATCAATCTACGCTTACGCTTCAAGATTATCTA 1119

RESULT 11
US-10-392-325-3
; Sequence 3, Application US/10392325
; Publication No. US2004006080A1
; GENERAL INFORMATION:
; APPLICANT: Tanaka, Hiroshi
; APPLICANT: Kayano, Toshiaki
; APPLICANT: Matsuo, Makoto
; APPLICANT: Kobayashi, Masatomo
; APPLICANT: Saito, Tamio
; APPLICANT: Sakamoto, Tomoaki
```



```
QY 60 LeuGluLeuMetAlaAsnLeuGluAenGluAlaLeuArgPhePheLysSerGlnSer 79
Db 320 ACGCACGATGACAAAGCCGAGTCGGAGGCGTCAGGTCTCTCCAGCAGCAGCCC 379
QY 80 GluLysAspArgAlaGlyProProAspPhePheGlyTyrGlySerLysArgIleGlyPro 99
Db 380 GACAAAGACCGCTCCGGCCCGGCTACCCGGTTCCGGTACGGCAGCAAGCGATCCGGTTC 439
QY 100 AnGlyAspValGlyTrpValGluTyrLeuLeuAsnThrAsn-----Pro 115
Db 440 AATGGCGACATGGGGTGGCTCGAGTACCTCTCCCTCCGCTGACACCGCTCGCTCGCC 499
QY 116 AspValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAla 135
Db 500 GACGCTGCACCGCTCCGCTCTCGCGGTC-----TTCCGGGCGC 538
QY 136 ValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMet 155
Db 539 GCTCTGAACGAGTACATCTCGGGGTGCGGAAGGTGGCGGTGCGGTGATGGAGCGATG 598
QY 156 AlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLys 175
Db 599 TCGAGGGGCTGGGCATTCGCGAGCGGACGCGCTGAGCGCGCTGGTGAACGGCGAAGG 658
QY 176 SerAspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsn 195
Db 659 AGCAGCAGGTGTTCCGCTGAACCACTACCCGCGCTGCGCGCTGCGAGGGCTCGGC 718
QY 196 ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSer 215
Db 719 TGCAGCGTCACCGGCTTCGCGAGCAGCACCGACCGCGAGCTGCTCTCCGCTCA 778
QY 216 AnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProPro 235
Db 779 AACGGCACGTCGCGCTCGAGATCGCGCTCCGGACGCGCAGTGGGTGTCGTCGCCCTCC 838
QY 236 AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg 255
Db 839 GACCGGAGCTCCTCTCTTCGTAAGCTGCGGAGCTCGTTTCAGGTTCTGACCAATGGAGG 898
QY 256 PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle 275
Db 899 TTCAAGAGCGTGAAGCACAGGTGGTGGCCACAGCCTAAAGTCTAGGGTTTCTTCATC 958
QY 276 TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys 295
Db 959 TACTTTGGAGGGCCACCCTTAGCACAGAGATTGCACCATTCACAGCTGCTGGGGAG 1018
QY 296 GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaIaIaTyrThr 315
Db 1019 GGAGAGCAGAGCTGTACAAAGAGTTTCATATGGGATGATACAAAGAGCTGCCTACAAA 1078
QY 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 1079 TCAAGGCTTGGAGACAAACAGGCTGGCCCGGTTTGGAAG 1117
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RESULT 13

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US-10-425-115-69575
; Sequence 69575, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 69575
; LENGTH: 1611
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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_163444C.1
US-10-425-115-69575

Alignment Scores:
Pred. No.:      8,42e-115      Length:      1611
Score:          957.50         Matches:    191
Percent Similarity: 70.75%      Conservative: 46
Best Local Similarity: 57.01%    Mismatches:  83
Query Match:      54.78%       Indels:     15
DB:               8           Gaps:         4

US-10-670-454-2 (1-331) x US-10-425-115-69575 (1-1611)

QY 1 MetValValLeuSerGln---ProAlaLeuAsnGlnPhePheLeuLeuLysProPheLys 19
Db 175 ATGGTGGTCTCGCCAAACCGCTCTCGTCGACCAAGATCCCGCTCTCGGTCCCGGGC 234
QY 20 SerThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsn 39
Db 235 CCCAGGGACAGCTTCTCGGAGTGCCTGCTGTCGACCTGTCAGCCAGCCGCGCGGGCGG 294
QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
Db 295 GCGATCGTCGACGCTCGAGCGCTTCGGGTCTTCAAGTCTCAAGTCTCAACCCAGCGCTGGCC 354
QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
Db 355 GCGGCCACCATGACAGGGCCGAGTCCGAGGCGCTCAGGTCTTTCGCGCAGCGCGAGGGC 414
QY 80 GluLysAspArgAlaGlyProProAspPheGlyTyrGlySerLysArgIleGlyPro 99
Db 415 GACAAGACCGCGCGCGCGCGGTACCGCTTCGGGTACGCGAGCAGCGATCGGGCTC 474
QY 100 AnGlyAspValGlyTrpValGluTyrLeuLeuAsnThrAsnProAspValIleSer 119
Db 475 AATGCGACATGGGTGGCTCGAGTACCTCTCTCTCGCGTGCAGCGCGCTGCTCTCC 534
QY 120 -----ProLysSerLeuCysIlePheArgGluAsnProHisPheArg 134
Db 535 GACGCTCGCCCGCTCCCTCCAGCGCGCG-----TTCGGG 570
QY 135 AlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeu 154
Db 571 ACGCGCTGAACGAGTACGTCGCGCGCTGCGGAAGTGGCGCGCGCTGCTGTGAGGGC 630
QY 155 MetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLysAspGlu 174
Db 631 ATGGCGGAGGGCTGGGCATTGCGGACGCGGACGCGCTGAGCTCCATGGTGAAGCGCGC 690
QY 175 LysSerAspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeu 194
Db 691 GGGAGCGACCAAGTGTTCGGGTGAACCACTACCCGCGCTGCGCGCGCTGCGAGGGCTG 750
QY 195 AsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArg 214
Db 751 GGCTCAGGGCCACCGGGCTTCGGCGAGCACACCGCCGCGAGATCATCTCCGTGCTCCG 810
QY 215 SerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThr---TrpValSerVal 233
Db 811 TCCAACGGCACCTCCGGCTGCGAGTCCGCGCTCCGCGACGGCGCGAGTGGGTCTCCG 870
QY 234 ProProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsn 253
Db 871 CCCTCCGACCGGACGCGCTTCTCGTTAAGTCGCGGACTCGTTGACGTTGAGTGTCTCC 930
QY 254 GlyArgPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSer 273
Db 931 GGGAGTTTCAGGAGGTGAAGCACCGGGTGGTGACCAACAGCGCTCAGTCCAGAGTTCC 990
QY 274 MetIleTyrPheGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMet 293
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Db      991 TTCACTTACTTCGCGGGCGCGCTGGGGCAGCGATGCGCCGCTCCGCGAGTGCTG 1050
      294 LeuLysGlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAla 313
      1051 GCGGAGGAGGAGGAGGAGCTGTACAGGAGTTTCACTGGGGCGAGTACAGAGGCGCGG 1110
      314 TyrThrSerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
      1111 TACAAGACGAGCTCGCGCACACACAGGCTGGGCCAGTTTGAGAAG 1155

RESULT 14
US-10-670-454-9
; Sequence 9, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-9

Alignment Scores:
Pred. No.: 1,57e-114 Length: 1008
Score: 953.00 Matches: 186
Percent Similarity: 70.12% Conservative: 44
Best Local Similarity: 56.71% Mismatches: 96
Query Match: 54.52% Indels: 2
DB: 8 Gaps: 1

US-10-670-454-2 (1-331) x US-10-670-454-9 (1-1008)

Qy      1 MetValValLeuSerGlnProAlaLeuAsnGlnPheLeuLeuLysProPheLysSer 20
      1 ATGGTAATTTGTTACAGCCAGCCAGTTTGTATGACCAACCTCTATGTTAATCCAAATATGC 60
      21 ThrProLeuPheThrGlyLeProValValAspLeuThrHisProAspAlaLysAsnLeu 40
      61 AAACCGCGTCCGGTTTTATCCCTGTTATAGACTTAAACGACTCAGATGCCAAACCCAA 120
      41 IleValAsnAlaCysArgAspPheGlyPheLysLeuValAsnHisGlyValProLeu 60
      121 ATCGTCAAGGCATGGAAGAGTTTGGGTTCTTCAAGTCATCAACCATGGGGTCCGACCC 180
      61 GluLeuMetAlaAsnGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
      181 GATCTTTTGACTCAGTTGGAGCAGAGCCATCACTCTTTGCTTTCATCCTCTCTC 240
      81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
      241 AAAGACAAAGCGGTCCACCTCAGCCGTTTGGTACGGTACTATAAAGGATTGGACCCCAAT 300
      101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
      301 GGTGACCTTGGCTGGCTGGAGTACATTCCTCTTAATGCTAATCTTTGCTTGGCTTGCCTCAC 360
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Qy      121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
      361 AAAACCCACCGCATTTTCCGGCACACCCCTCAATTTTTCAGAGAGGCGAGTGGAGAGTAC 420
      141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
      421 ATTTAAGAGATGAAGAGATGTCGAGCAATTTCTGGAATATGGTAGAGAGAGCTAAG 480
      161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
      481 ATAGAGCCAAAGGAGAGCTCAGCGCTTTGGTGAAGGTGAAGAAAGTATTGCTGCTCG 540
      181 ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
      541 AGAATGACCATTTACCCGAGAGGAGAGACTCCGGTC-----AAGGAAGAGATTGGG 594
      201 PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly 220
      595 TTCGTGAGCACACTGATCCACAGTTGATATCATCTGCTCAGATCAACGACACAGAGGGT 654
      221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
      655 TTGCAAAATCTGTCAAAAGATGGAACATGGGTGTGATTTACACCTGATCCTCTCTTTC 714
      241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
      715 TTCGTTCTTGTGGAGATACTCTTCAGGTGATGACAAACGGAAGATTCACAGAGTGTGAA 774
      261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
      775 CATAGAGTGGTGACAAATACAAAGAGGTCAAGGATTCGATGATCTACTTCGAGGTCTCT 834
      281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
      835 CCTTTGAGCGAGAGATTGCACCATTTATCATGCTCTGTGCCCAAGCAAGATGATGCTCT 894
      301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
      895 TATAATGAGTTTACTTGGTCTCAATACAAAGTTATCTGCTTACAAAACTTAAGCTTGGTGAC 954
      321 AsnArgLeuAlaProPheGlnLys 328
      955 TATAGGCTTGGTCTCTCTTTGAGAAA 978

RESULT 15
US-10-259-194A-141
; Sequence 141, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghassemlian, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: PatentList.pl version 3.0.4 (c) 2001 Syngenta
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; SEQ ID NO 141
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-194A-141

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Alignment Scores:
Pred. No.: 2,93E-114 Length: 927
Score: 950.50 Matches: 186
Percent Similarity: 71.21% Conservative: 49
Beat Local Similarity: 56.36% Mismatches: 70
Query Match: 54.38% Indels: 25
DB: 6 Gaps: 3

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US-10-670-454-2 (1-331) x US-10-259-194A-141 (1-927)

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QY 1 MetValValLeuSer---GlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLys 19
DB 1 ATGGTGGTTCTCGCTGGCCCGCCCGCTCGATCATCATCCCGCTGCTGAGGTGCGCGGAC 60
QY 20 SerThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsn 39
DB 61 CCGGGCGACGTCTTTCGGGGTGGCGGTGCTGCGACCTCGGCGAGCCCGCGCGCGGAGG 120
QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValPro 59
DB 121 GCCGTGGTGGACGCTCGCGGCGGTACGGGTCTTCAAGGTGCTCAACCAACCGCGTGGCC 180
QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
DB 181 ACGGACACATGACAGCCGAGTGGAGGCGCTCAGGTCTCTCCCGACGCGAGCCC 240
QY 80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyPro 99
DB 241 GACAGGACCGCTCCGGCGCGCTACCGCTTCCGGTACGGAGCGGATCGGGTTC 300
QY 100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSer 119
DB 301 AATGGCGACATGGGTGGTTCGAGTACCTCTC----- 333
QY 120 ProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsn 139
DB 334 -----AGGCGCGCTCTGAACGAG 351
QY 140 TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeu 159
DB 352 TACATCTCGGGGTGCGAAGGTGGCGGTGCGGGTATGAGCGGATGCGAGGGGCTG 411
QY 160 GlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCys 179
DB 412 GGCATTGCGCAGCGGACGCGCTGAGCGCGTGGTGACGGCGAGGGAGCGACCGAGGTG 471
QY 180 PheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuVal 199
DB 472 TTCGCGTGAACCACTACCCCGCGTCCCGCGCTGCGAGGGCTCGGCTGCGAGCGTACC 531
QY 200 GlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSer 219
DB 532 GGCCTCGGCGAGCACACCGCGAGCTCGCTCCGCTCCTCAACCGGCGAGTCC 591
QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSer 239
DB 592 GGCCTGCAGATCGCGTCCCGAGCGGCGAGTGGGTGCTCGTCCCTCCGACCGGACTCC 651
QY 240 PhePheIleAsnValGlyAspAlaLeu---GlnValMetThrAsnGlyArgPheLysSer 258
DB 652 TTCCTTCGTCACGCTCGCGACTCGTTGCGAGCAGGTTCTGACCAATGGGAGGTTCAGAGC 711
QY 259 ValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGly 278
DB 712 GTGAGCACAGGGTGGTGGCCACACGCTTAAGTCTAGGGTTCTTCATCTACTTTGGA 771
QY 279 GlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlu 298

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DB 772 GGGCCACCGTTAGCACAGAGGATTGCACCATTTGCCACAGCTGCTGGGGGAGGAGCGAG 831
QY 299 CysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeu 318
DB 832 AGCCTGTACAAGGAGTTTACATGGGATGAGTACAAGAAGGCTGCCTACAAATCAAGGCTT 891
QY 319 AlaAspAsnArgLeuAlaProPheGlnLys 328
DB 892 GGAGACAACAGGCTGCGCCAGTTTGAGAAG 921

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Search completed: December 28, 2005, 05:05:07
Job time : 984 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2005, 01:42:45 ; Search time 786 Seconds
(without alignments)
220.763 Million cell updates/sec

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Perfect score: 1748
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Searched: 4172979 seqs, 262114271 residues

Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA_New.*

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9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	325.5	18.6	1017	US-11-152-892-5
2	288	16.5	1011	Sequence 5, Appli
3	173	9.9	3861	Sequence 3, Appli
4	169.5	9.7	2171	Sequence 2, Appli
5	89.5	5.1	967	Sequence 1, Appli
6	84	4.8	193084	Sequence 3, Appli
7	83.5	4.8	1243	Sequence 82, Appli
8	82.5	4.7	5515	Sequence 50357, A
				Sequence 14, Appli

c	9	82.5	4.7	5515	7	US-11-055-309A-2	Sequence 2, Appli
c	10	82.5	4.7	5982	7	US-11-034-771-1	Sequence 1, Appli
c	11	82.5	4.7	153142	7	US-11-121-086-27	Sequence 27, Appli
c	12	81.5	4.7	40000	6	US-10-995-561-13513	Sequence 13513, A
c	13	81	4.6	3587	6	US-10-501-675-8	Sequence 8, Appli
c	14	80.5	4.6	1535	6	US-10-750-185-34363	Sequence 34363, A
c	15	80.5	4.6	15804	6	US-10-995-581-13294	Sequence 13294, A
c	16	80.5	4.6	16963	6	US-10-995-561-13467	Sequence 13467, A
c	17	80.5	4.6	24446	6	US-10-995-561-13436	Sequence 13436, A
c	18	80.5	4.6	175416	7	US-11-121-086-43	Sequence 43, Appli
c	19	79.5	4.5	972	7	US-11-058-817A-1	Sequence 1, Appli
c	20	79	4.5	751	9	US-11-082-389-53	Sequence 53, Appli
c	21	79	4.5	1111	6	US-10-750-185-60397	Sequence 60397, A
c	22	79	4.5	1287	9	US-11-082-389-51	Sequence 51, Appli
c	23	78	4.5	595	6	US-10-980-388-41	Sequence 41, Appli
c	24	78	4.5	1082144	7	US-11-117-187-211	Sequence 211, App
c	25	77.5	4.4	861	6	US-10-467-657-2959	Sequence 2959, Ap
c	26	77	4.4	810	6	US-10-467-657-1629	Sequence 1629, Ap
c	27	76.5	4.4	197096	7	US-11-121-086-107	Sequence 107, App
c	28	76.5	4.4	209822	6	US-10-995-561-13198	Sequence 13198, A
c	29	76	4.3	207908	7	US-11-112-908-21	Sequence 21, Appli
c	30	75.5	4.3	98862	7	US-11-121-086-76	Sequence 76, Appli
c	31	75.5	4.3	215308	7	US-11-121-086-77	Sequence 77, Appli
c	32	75	4.3	2858	6	US-10-750-185-34315	Sequence 34315, A
c	33	74.5	4.3	1245	6	US-10-467-657-7773	Sequence 7773, Ap
c	34	74.5	4.3	2407	6	US-10-750-185-33843	Sequence 33843, A
c	35	74.5	4.3	1125000	6	US-10-995-561-13286	Sequence 13286, A
c	36	74	4.2	625	7	US-11-000-463-554	Sequence 554, App
c	37	74	4.2	970	7	US-11-058-817A-5	Sequence 5, Appli
c	38	74	4.2	1952	6	US-10-750-185-62955	Sequence 62955, A
c	39	74	4.2	215308	7	US-11-121-086-77	Sequence 77, Appli
c	40	73.5	4.2	1449	7	US-11-055-822-401	Sequence 401, App
c	41	73.5	4.2	2119	6	US-10-927-641-92	Sequence 92, Appli
c	42	73.5	4.2	2295	7	US-11-000-463-590	Sequence 590, App
c	43	73	4.2	1161	6	US-10-750-185-64816	Sequence 64816, A
c	44	73	4.2	1359	6	US-10-750-185-55071	Sequence 55071, A
c	45	73	4.2	1443	6	US-10-750-185-31989	Sequence 31989, A

ALIGNMENTS

RESULT 1
US-11-152-892-5
; Sequence 5, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1014)
US-11-152-892-5

Alignment Scores:
Pred. No.: 2,469-29 Length: 1017
Score: 325.50 Matches: 82
Percent Similarity: 46.62% Conservative: 63
Best Local Similarity: 26.37% Mismatches: 103
Query Match: 18.62% Indels: 63

DB: 7 Gaps: 12

US-10-670-454-2 (1-331) x US-11-152-892-5 (1-1017)

QY 27 IleProValValAspLeuThr-----HisProAspAla 37

Db 124 CTTCTCTGTGATTGACGTCAAGCGTTTGATTGATGAGCCGAGGAGGAGAGAGAAATGT 183

QY 38 LysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGly 57

Db 184 AAGAAAGCGATTTCGAGAGACTTCGAGGAGTGGGGATTTTTCAAGTGATAAACCATGGA 243

QY 58 ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePhe----- 74

Db 244 ATATCAATCGATGTGTTGGAGAAGATGAGACAAGCAAAATTAGGGTCTTTAGAGAGCCT 303

QY 75 -----LysGlySerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyr 92

Db 304 TTTGACACAGAAAAGTAAGTCGAGAGAAATTTTCCGCCGG-----AGTTACCGGTGG 354

QY 93 GlySerLysArgIleGlyProAsnGlyAspValGlyTrpValGluTyrLeuLeu----- 110

Db 355 GGAACCGCGTCAGCCACTTCTATCCGCGAGCTTCTTGGTCAGAAAGCTTTTCATGTTC 414

QY 111 -----LeuAsnThrAsnProAspValIleSerProLysSerLysCysIlePheArg 127

Db 415 ATGACAGATATTCTTGACAAACAGGACTTTACTACTCTCAGCTCA----- 459

QY 128 GluAsnProHisPheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMet 147

Db 460 -----ACAATGAGAAATTTGCTTCGGAATCAGAGGCATTA 495

QY 148 CysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeu 167

Db 496 GCATATATGTTGCGAGAGTCTTCGCAGAAAACAGCAGACAAA----- 540

QY 168 SerArgLeuLeuLysAspGlu---LysSerAspSerCysPhe---ArgLeuAsnHisTyr 185

Db 541 TCAAGTTTCTCAAAGAAACTGTGTGAGAAATACATGTTATCTAAGGATGAACCGATAT 600

QY 186 ProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThr 205

Db 601 CCACCTTGTTCCAAACCATCG-----GAGGTGTACGGATTAAATGCCACATACG 648

QY 206 AspProGlnIleIleSerValLeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeu 225

Db 649 GACGTGATTTCCTTACAACTTGATCAAGATCAAGTCGGAGGACTCCAACCTC---ATC 705

QY 226 ThrAspGlyThrTrpValSerValProAspGlnThrSerPhePheIleAsnValGly 245

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QY 246 AspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLysHisArgValLeuAla 265

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QY 266 AspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyProAlaLeuSerGluAsn 285

Db 826 AACCCAAAGGTGGAGATTCCTCAACGCTTATTTTATGTGTCCATCATACGACGCCGT 885

QY 286 IleAlaProLeuProSerValMetLeuLysGlyGluGluCys-----Leu 300

Db 886 ATA-----GAGTGTTCAGTGATCGTCTGTCT 912

QY 301 TyrLysGluPheThrTrpCysGluTyrLysLys 311

Db 913 TATAGAAATTTTCAGCTTCAGAGAATTTCAGACA 945

RESULT 2

US-11-152-892-3

; Sequence 3, Application US/11152892

; Publication No. US20050251883A1

; GENERAL INFORMATION:

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; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1008)
US-11-152-892-3

Alignment Scores:
Pred. No.:          9,54e-25          Length:          1011
Score:              288.00            Matches:         79
Percent Similarity: 43.95%            Conservative:    59
Best Local Similarity: 25.16%          Mismatches:     110
Query Match:        16.48%            Indels:         66
DB:                  7                Gaps:          11

US-10-670-454-2 (1-331) x US-11-152-892-3 (1-1011)

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Qy      39  ---AsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGly 57
Db      178 GTGAAACAAATGGTTGCAGCTCGGAAGAGTGGCGATTTTTTCAAATTTGTGAACCATGGA 237
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      58  ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSer 77
Db      238 ATTCCTCCAAAGACGCTCTTTGATGATGATGCTCTCGAAGAGAGAAACTCTTTGACCAACCT 297
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      78  GlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyxGlySerLysArgIle 97
Db      298 TTTTCTGTGAAGTCAGAGAACGTTTTCGGAC---TTATCGAAGATAGTTACCGTTGG 354
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      98  GlyProAsnGlyAspValGlyTyrpValGluTyrLeuLeuLeuAsnThrAsnProAspVal 117
Db      355 GGA-----AACCCTAGCGCC 369
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      118  IleSerProLysSerLeuCysIle-----125
Db      370 ACTTCTCCGCTCAGTACTCCGTTTCGGAAGCGTTTCACATCATCTTTTCAGAGGTTTCA 429
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      126  ---PheArgGluAanProHisHisPheArgAlaValGluAsnTyrIleThrAlaVal 144
Db      430 AGGATTCTGATGATCGGCACAACTCGAACAAATCGTTGAAGCGTATGTGCAGAGATA 489
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      145  LysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArg 164
Db      490 GCTCGAGTGGCCACAAATGATATGTGAATACTCTGGGG-----AAACAAGTG 534
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      165  AsnThrLeuSerArgLeuLeuLysAsp-----GluLysSerAspSerCysPheArgLeu 182
Db      535 AACGTGAGTTCGGAGTATTTTCGAAACAACTTTTGTAGCTTGAATAACAGTTTCTTAAGGCTC 594
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Qy      183  AsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGlyPheGly 202
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Db 643 CCTATACGATCAAGTTTCTCACTATCTCTCAAGATCAAAATCGGAGGTTAGA 702
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Qy 243 AanValGlyAspAlaLeuGlnValMetThrAnGlyArgPheLysSerValLysHisArg 262
Db 760 AACATTTGGGGATATGTTTCAGGCATCGAGTAAATGGAGTGATACCAAGCGTGAGACATAGA 819
Qy 263 ValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyPheGlyGlyProAlaLeu 282
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Qy 283 SerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu----- 300
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Qy 301 -----TyLysGluPheThrTrpCysGluTyLysLys 311
Db 907 CCAAGAAGATATAGAAGATTTCAGTTTCAGAGGATCAAAAGAG 948

RESULT 3
US-11-152-892-2
; Sequence 2, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Arabidopsis
US-11-152-892-2

Alignment Scores:
Pred. No.: 9,08e-10 Length: 3861
Score: 173.00 Matches: 55
Percent Similarity: 36.12% Conservative: 40
Best Local Similarity: 20.91% Mismatches: 61
Query Match: 9.90% Indels: 107
DB: 7 Gaps: 9

US-10-670-454-2 (1-331) x US-11-152-892-2 (1-3861)
Qy 135 AlaValValGluAsnTyrlleThrAlaValLysAsnMetCysTyrlleAlaValLeuGluLeu 154
Db 3066 TCAACAATCGAGAAATTTCTCGGAATCAGAGGCATTAGCATATATGTGGCAGAGGTT 3125
Qy 155 MetAlaGluGlyLeuGlylleArgGlnArgAnThrLeuSerArgLeuLeuLysAspGlu 174
Db 3126 CTTGCAGAAAAATCTCGA-----CAAAAT-----TCAAGTTTCTTCAAGAAAAAC 3170
Qy 175 ---LysSerAspSerCysPhe---ArgLeuAsnHisTyrlleProCysProGluValGln 192
Db 3171 TGTGTGAGAAATACATGTTTATAGGATGAGACCGATATCCACCTTGTCCCAACCATCG 3230
Qy 193 AlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerVal 212
Db 3231 -----GAGGTGTACGGATTATGCGCACACGACGAGTGAATTCCTCACAATC 3278
Qy 213 LeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSer 232

```

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Db 3279 TTGTATCAAGATCAAGTCGGAGGACTCAACTT---ATCAAGACAAATAGATGGATCGCT 3335
Qy 233 ValProAspGlnThrSerPhePheleAenValGlyAspAlaLeuGlnVal----- 250
Db 3336 GTTAAACCTAATCTCTAAAGCTCTCATTAATCAATATGGTGGTACTTATTTTCAAGTAATGAG 3395
Qy 250 ----- 250
Db 3396 CTTTATTATTATGTCATTCTACCATTTACCATTTATATATCATTTATCCGGAGCTTACAAATAGTT 3455
Qy 250 ----- 250
Db 3456 TGGTATTTTATGTTTGTATGTTTGGAGGATTTAAACAAATTTGTTTCATACGCATGCA 3515
Qy 250 ----- 250
Db 3516 TGATCAATAATTAATAAATGTGGATTTCCTATAAAGATAACATCTAAGGCAATGTATTAAA 3575
Qy 251 -----Met-ThrAsnGln 254
Db 3576 AATGCTTTTAAATTTACTAGATTGTACTTATATATGTGTTGTTAGGCATGGAGCAATGG 3635
Qy 254 YargPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMe 274
Db 3636 CATGTACAAAGTGTGTAACACCGTGTATGATGACGACCCAAAGGTGGAGAGATTCTCAAC 3695
Qy 274 tIleTyPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
Db 3696 GCGTTATTTTATGTGTCATCATACGACGCGCTTATA----- 3732
Qy 294 uLysGlyGluGluCys-----LeuTyrllysGluPheThrTrpCysGluTy 309
Db 3733 -----GAGTGTTCAGTGATGCTCTCTTATAGAAATTTTCAGCTTCAGAGAAAT 3782
Qy 309 tLysLys 311
Db 3783 CAGACAA 3789

RESULT 4
US-11-152-892-1
; Sequence 1, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Arabidopsis
US-11-152-892-1

Alignment Scores:
Pred. No.: 1e-09 Length: 2171
Score: 169.50 Matches: 74
Percent Similarity: 30.84% Conservative: 54
Best Local Similarity: 17.83% Mismatches: 96
Query Match: 9.70% Indels: 191
DB: 7 Gaps: 14

US-10-670-454-2 (1-331) x US-11-152-892-1 (1-2171)
Qy 27 ileProValValAspLeuThrHis-----ProAspAlaLys----- 38

```


Db 118 CTTCTGTGTCATCTCAGCCATCTAACTAGTGGTGAGAGGTCAAAACGCAAAAGATGT 177
 Qy 39 ---AsnLeuIleValAsnAlaCysArgAspPheGlyPhePhePheLeuValAsnHisGly 57
 Db 178 GTGAACAACAAATGGTTCAGCTCGAAGAGATGGGGATTTTTCAAATTTGTGAACCATGGA 237
 Qy 58 ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePhePheLeuValSer 77
 Db 238 ATTCCCAAGACGCTTTTGAGATGATGCTCCTCGAAGAGAGAACTCTTTGACCAACCT 297
 Qy 78 GlnSerGluLysAspArgAla-----Gly 85
 Db 298 TTTTCTGTGAAGTCAGAGAACGCTTTTCGGACTTATCGAAGAAATAGTTACCGTTGGGA 357
 Qy 86 ProPro-----AspProPheGlyTyrGly----- 93
 Db 358 AACCCCTAGCGCCACTTCTCCCGCTCAGTACTCCGTTTCGGAGCGTTTCACATCATCTTT 417
 Qy 94 -----SerLysArgIleGlyProAsnGlyAspValGlyTyrValGluTyr----- 108
 Db 418 TCAGAGGTTTCAAGGATTTCTGATGATCGCAACAACCTCAGGTTTTTTAATTATAGATT 477
 Qy 108 ----- 108
 Db 478 TTTATCTTTATTGATTGAATTTCTGCTCATGAACCCCTAATCTTGAATTTGCTAGTTG 537
 Qy 109 -----LeuLeuLeuAsnThrAsnProAspValIleSerProLysSer----- 122
 Db 538 TTTCTTTTAAATATAATGACTCACTGATATCGTTTCAGGGAAAGTTCTTAGCCAGTC 597
 Qy 122 ----- 122
 Db 598 ATACTCGTTTCCCTCAGTTTCATCAATCAATAATTTCTAGATATCTTTTATGAATTC 657
 Qy 123 LeuCysIlePheArg----- 127
 Db 658 TTGCGAGTATATAGATTTTAAATATTTGGAGTGAATTTGGTTTGTCTGAAGATTTCAAT 717
 Qy 127 ----- 127
 Db 718 TTTTGAATGAATTTGTTAGGTCTTTTGGAGATCAAGCAAGTTTCACATGCTTGTAT 777
 Qy 127 ----- 127
 Db 778 ATAGTAGTATTATAGAAACACTTATAAATCTTTATGTTTAAAGAAAACCTTTCATACAGT 837
 Qy 127 ----- 127
 Db 838 TCATATATAGAGATATATTGTTAGTTATACATACAAAAATAAAAAAATAACAAGATCATAA 897
 Qy 128 -----GluAsnProHis----- 132
 Db 898 ATCATTATATACATATATATAGATAGATGAATAACCGTTACATTAATTAATTTCTATTTCT 957
 Qy 133 ---PheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaVal 151
 Db 958 TTTTACAGAACATCGTTGAAACGATATGTCGAAGAGATAGCTCGAGTGGCACAATGATA 1017
 Qy 152 LeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeu 171
 Db 1018 TGTGAATAACTGGG-----AAACAAGTGAACGTGAGTTGCGAGTATTTTC 1062
 Qy 172 LysAsp-----GluLysSerAspSerCysPheArgLeuAsnHisTyrProCysPro 189
 Db 1063 GAAAAACATTTTGGAGCTTGAAACAGTTTCTAAGGCTCAATTAAGTACCATCT----- 1116
 Qy 190 GluValGlnAlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIle 209
 Db 1117 -----AGTGTTTTGGTCTGAGTGTGTTGGTTTGGTTCTCATACCGATACAACTTTT 1170
 Qy 210 IleSerValLeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThr 229
 Db 1171 CTCACATATCTCTCAAGATCAATCGGAGGTTAGAAATTG-----GAAATAATATGACAA 1227

Qy 230 TrpValSerValProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGln 249
 Db 1228 TGGATCAGCGTAAACCTTGTGGAGCCCTTACAGTCAACATTTGGGATATGTTTCAG 1287
 Qy 250 ValMetThrAsn-----GlyArgPheLysSerValLys 260
 Db 1288 GTAATTACTTCTACCCCTTTGATTTTCAAGCTTCAAGTCCATTAA 1332
 RESULT 5
 US-11-058-817A-3/c
 ; Sequence 3, Application US/11058817A
 ; Publication No. US20050262580A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Petrukhin, Konstatin
 ; APPLICANT: Webber, Andrea L.
 ; TITLE OF INVENTION: Transgenic Mouse with a targeted
 ; TITLE OF INVENTION: deletion of ELOVL4 Gene
 ; FILE REFERENCE: 21550
 ; CURRENT APPLICATION NUMBER: US/11/058,817A
 ; CURRENT FILING DATE: 2005-02-16
 ; PRIOR APPLICATION NUMBER: 60/545,358
 ; PRIOR FILING DATE: 2004-02-18
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 967
 ; TYPE: DNA
 ; ORGANISM: human
 US-11-058-817A-3
 Alignment Scores:
 Pred. No.: 1,81 Length: 967
 Score: 89.50 Matches: 72
 Percent Similarity: 33.33% Conservative: 39
 Best Local Similarity: 21.62% Mismatches: 103
 Query Match: 5.12% Indels: 119
 DB: Gaps: 16

US-10-670-454-2 (1-331) x US-11-058-817A-3 (1-967)

Qy 12 PhePheLeuLeuLysProPheLysSerThrProLeuPheThrGlyIleProValValAsp 31
 Db 925 TTTTCTGCTTTTTCCTTTTCTATCATGAGTGTGTTTCT- - - - -GAT 881
 Qy 32 LeuThrHisProAspAlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhe 51
 Db 880 TTGCTCACACCAATTTGCTGAAATACCATTCATGCGTGTGTTTCCAGCTTTTGGTTTC- - - 824
 Qy 52 LysLeuValAsnHisGlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeu 71
 Db 823 - - - - -TTAGGCTCTTTGTATGTC 806
 Qy 72 ArgPhePheLysSerGlnSerGluLysAspArgAlaGly- - - - -ProProAsp 88
 Db 805 CGAATGTACAGAAAGAGAAATATGAAGCTGATTGTCATAGGCAATTAGAGCCCGAGTGCAT 746
 Qy 89 ProPheGlyTyrGlySerLysArgIleGly- - - - -ProAsnGly- - - - - 101
 Db 745 CCATTTGGGGAAGGGGCGAGTCAGTGTAAAGAGACAGTGCCTGTGCCAATGTCACATG 686
 Qy 102 AspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspVal- - - - -IleSerPro 120
 Db 685 GAATTGAATCAGTTGCAACATAGTCAGGTATCGTTTCCACCAAGATATTTCTGATATCCA 626
 Qy 121 LysSerLeuCys- - - - -IlePheArgGluAsnProHisPheArgAlaValVal 137
 Db 625 TGGGCCAAATGCAGTTTAACCCATAGTATGAGTACATAATCAC- - - - - 584
 Qy 138 GluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGlu 157
 Db 583 - - - - -ATGGATAAA 575


```

RESULT 6
US-11-121-086-82
; Sequence 82, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82
; LENGTH: 193084
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-82

Alignment Scores:
Pred. No.:      2.96e+04      Length:      193084
Score:          84.00        Matches:     33
Percent Similarity: 42.62%    Conservative: 19
Best Local Similarity: 27.05%   Mismatches:  37
Query Match:      4.81%       Indels:      33
DB:                7         Gaps:        5

US-10-670-454-2 (1-331) x US-11-121-086-82 (1-193084)

Qy      106 ValGluTyrLeuLeuAsnThrRanProAspValIleSerProLysSerLeuCysIle 125
      ||| ::: |||||
Db      68088 GTGAGCATTCATCAGCAATAACAATAGCTCTGCACATTAAAGTATATTCT----- 68138

Qy      126 PheArgGluAsnProHisPheArgAlaValAluAsnTyrIleThrAlaVal--- 144
      ||||| :|||||

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Db	68139	-----	GAACCTCACCACTTCTCAGCCATAATCAAGGCACCATATCGCACTTTGA	68189
QY	145	-----	---LysAsnMetCysTyr-AlaValLeuGluLeuMetAlaGluGlyLeuGlyI1	161
Db	68190	CTACTGCAACAGCTTCTTATCTATTCTCTATTCTTCAACTCTTGCTTCTCT	-----	68241
QY	161	eArgGlnArgAsnThrLeuSerArgLeuLeuLeuAspGluLysSerAspSerCysPheAr	181	
Db	68242	-----	TAGATCCTGCTCTCCAATCAGCAATCTGATTTCATTTCTTCAG	68282
QY	181	gLeuAenHisTyrProProCysProGluValGlnAlaLeuAenArgAenLeuValGlyPh	201	
Db	68283	AATGAATCATGTCTCTGTTGTACTCAAAAGTATACATT	-----	68322
QY	201	eglyGluHisThrAspProGlnIleIleSerVal---	LeuArgSerAenSerThrSerGl	220
Db	68323	-----	CCCTCTATCCTTCTTGTTCATTAAACTCTAACACACTGAATT	68366
QY	220	yLeu 221		
Db	68367	CCTT	68370	
RESULT 7				
US-10-750-185-50357/c				
; Sequence 50357, Application US/10750185				
; Publication No. US20050260603A1				
; GENERAL INFORMATION:				
; APPLICANT: MMI GENOMICS, INC.				
; APPLICANT: DENISE, Sue K.				
; APPLICANT: KERR, Richard				
; APPLICANT: ROSENFELD, David				
; APPLICANT: HOLM, Tom				
; APPLICANT: BATES, Stephen				
; APPLICANT: FANTIN, Dennis				
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS				
; FILE REFERENCE: MM1100-2				
; CURRENT APPLICATION NUMBER: US/10/750,185				
; CURRENT FILING DATE: 2003-12-31				
; PRIOR APPLICATION NUMBER: US 60/437,482				
; PRIOR FILING DATE: 2002-12-31				
; NUMBER OF SEQ ID NOS: 64922				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 50357				
; LENGTH: 1243				
; TYPE: DNA				
; ORGANISM: Bovine 19866880918438				
US-10-750-185-50357				
Alignment Scores:				
Pred. No.: 14.5 Length: 1243				
Score: 83.50 Matches: 47				
Percent Similarity: 34.72% Conservative: 20				
Best Local Similarity: 24.35% Mismatches: 69				
Query Match: 4.78% Indels: 58				
DB: 6 Gaps: 7				
US-10-670-454-2 (1-331) x US-10-750-185-50357 (1-1243)				
QY	133	PheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeu	152	
Db	1064	TTCCAGAATGCTTTTCTCGTTATTTTACAATCATGTAATAAGCGCTGCCAATGTCAGCTT	1005	
QY	153	GluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSer-	168	
Db	1004	CAGCTTACTATTGAGAGTAAATAATTAAGACAGTCTCTATAANTTTCGGTTTGAAAACC	945	
QY	169	ArgLeuLeuLysAspGluLysSerAspSerCysPheArgLeuAenHis-	184	
Db	944	AGCCTTATCCACCAAGAGTTCCTCGCTCAGAGGGCAGTACTGAGCATGATGAGCCCCCA	885	
QY	185	-----	TyrProProCysPro-	190
Db	894	AGTCAAGACAGAAGCCAACTCTGCTCTCTCCCTCCCAACCCCAATTCGTTCAGTCTGAG	825	

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/ FILE REFERENCE: WML100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 50357
/ LENGTH: 1243
/ TYPE: DNA
/ ORGANISM: Bovine 19866880918438
US-10-750-185-50357

Alignment Scores:
Pred. No.: 14.5 Length: 1243
Score: 83.50 Matches: 47
Percent Similarity: 34.72% Conservative: 20
Best Local Similarity: 24.35% Mismatches: 69
Query Match: 4.78% Indels: 58
DB: 6 Gaps: 7

US-10-670-454-2 (1-331) x US-10-750-185-50357 (1-1243)

Qy 133 PheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeu 152
Db 1064 TTTCCAGAATGCTTTTTCGTGGTTATTTTACAATCATTTGAATGAAGCTTGCCAATGTCAGCTT 1005
Qy 153 GluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSer- 168
Db 1004 CAGCTTACTATTGAGAGTAAATAATATTGAACAGCTCTCATTAATTTCCGTTTGAAACC 945
Qy 169 ArgLeuLeuLysAspGluLysSerAspSerCysPheArgLeuAsnHis- 184
Db 944 AGCCYTTATCCACAGAGTTCCTCGGCTCAGAGGGCAGTACTGAGCATGATGAGCCCCA 885
Qy 185 -----TyrProProCysPro-----Glu 190
Db 894 AGTCAAGACAGAGCAAGCCAACTCTGGCTCTCTCCCTCCCAACCCCAATTCGTTCAGTCTGAG 825

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QY 110 LeuLeuAenThrAsnProAspValIleSerProLysSerLeuCyAlpPheArgGluAen 129
 Db 4488 TCGCTGGGCACACGGCGCGCTGGTG---CCACGGCAGCGCTGCACCTTCTCCACCAGC 4432
 QY 130 ProHisHisPheArgAlaValValGluAen----- 139
 Db 4431 CGGCGCCACCTGGCGCTGCATGTCCTCCACGAGGCTCGAACACAGCTTTGAGGCGGCGC 4372
 QY 140 ---TyrIleThrAlaValLysAenMetCysTyrAlaValLeuLeuMetAlaGluGly 158
 Db 4371 TGGAGGCGCTGGCGCTGCAGGCGTATCTGCTGGGC-----TGCTCTCCAG- 4325
 QY 159 LeuGlyIleArgGlnAraAenThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178
 Db 4324 CTTGGCGGCGACCTCGGCACCTGCTCTTACCTCGTCCAGGCGTCCGGGTCGGCT 4265
 QY 179 CysPheArgLeuAen-----HisTyrProCysProGluValGlnAlaLeuAenArg 196
 Db 4264 GCCCATCTCTCCATCCGCGCGCGCAGCGCTCGCCCGCAGGCTGGCGCGCTCTCTGTAG 4205
 QY 197 AenLeuValGlyPheGlyGluHisThr 205
 Db 4204 CGGCTGGCGCGCGCAGGAGCCACAGT 4178

RESULT 10
 US-11-034-771-1/c
 ; Sequence 1, Application US/11034771
 ; Publication No. US20050277129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aerssens, Jeroen
 ; APPLICANT: Athanasios, Maria
 ; APPLICANT: Brain, Carlos
 ; APPLICANT: Cohen, Nadine
 ; APPLICANT: Dain, Bradley
 ; APPLICANT: Denton, R. Rex
 ; APPLICANT: Judson, Richard S.
 ; APPLICANT: Ozdemir, Vural
 ; APPLICANT: Reed, Carol R.
 ; TITLE OF INVENTION: APOE Genetic Markers Associated with Age of Onset of Alzheimer's
 ; FILE OF INVENTION: Disease
 ; FILE REFERENCE: 2300.0130801
 ; CURRENT APPLICATION NUMBER: US/11/034,771
 ; CURRENT FILING DATE: 2005-01-14
 ; PRIOR APPLICATION NUMBER: US 60/538,590
 ; PRIOR FILING DATE: 2004-01-22
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1
 ; LENGTH: 5982
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1102)..(1102)
 ; OTHER INFORMATION: n is 't' or 'c'
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1641)..(1641)
 ; OTHER INFORMATION: n is 'c' or 'g'
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2476)..(2476)
 ; OTHER INFORMATION: n is 'g' or 'a'
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4415)..(4415)
 ; OTHER INFORMATION: n is 't' or 'c'
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4553)..(4553)
 ; OTHER INFORMATION: n is 'c' or 't'
 US-11-034-771-1

Alignment Scores:
 Pred. No.: 215 Length: 5982
 Score: 82.50 Matches: 40
 Percent Similarity: 36.69% Conservative: 22
 Best Local Similarity: 23.67% Mismatches: 64
 Query Match: 4.72% Indels: 44
 DB: 7 Gaps: 7
 US-10-670-454-2 (1-331) x US-11-034-771-1 (1-5982)
 QY 75 LysLysSerGlnSerGluLysAspArgAla----- 84
 Db 5151 AGGAATACACAGGAGGAGCGCAGCAGATGCGTGAACTTTTATTAACTAG 5092
 QY 85 GlyProProAspProPheGlyTyrGlySerLysArgIle----- 97
 Db 5091 GGTCCACCCAGGAGGAGCGCTGGGCGGGGACAGGCTCCCCGTGCAGGCTGCGCGA 5032
 QY 98 GlyProAsnGlyAspValGlyTyr-----ValGluTyrLeu 109
 Db 5031 GGCAGGAGCAGCGGCTGGCGTGGCGTGCATGCTGCAGGCTTCGGCGTTTCAGTGTG 4972
 QY 110 LeuLeuAenThrAsnProAspValIleSerProLysSerLeuCyAlpPheArgGluAen 129
 Db 4971 TCGCTGGGCACAGGCGCGCGCTGGTG---CCACGGCAGCGCTGCACCTTCTCCACCAGC 4915
 QY 130 ProHisHisPheArgAlaValValGluAen----- 139
 Db 4914 CGGCGCCACTGGCGCTGCATGCTTCCACAGGCGCTCGAACACAGCTCTTGAAGCGGCGC 4855
 QY 140 ---TyrIleThrAlaValLysAenMetCysTyrAlaValLeuLeuMetAlaGluGly 158
 Db 4854 TGAAGGCGCTGGCGCTGCAGGCGTATCTGCTGGGC-----TGCTCTCCAG- 4808
 QY 159 LeuGlyIleArgGlnAraAenThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178
 Db 4807 CTTGGCGGCGCACCTCCCGCCACCTGCTCTTACCTCGTCCAGGCGGTGCGGGTCCGGCT 4748
 QY 179 CysPheArgLeuAen-----HisTyrProCysProGluValGlnAlaLeuAenArg 196
 Db 4747 GCCCATCTCTCCATCCGCGCGCGCAGCGCTCGCCCGCAGGCGCTCTCTGTAG 4688
 QY 197 AenLeuValGlyPheGlyGluHisThr 205
 Db 4687 CGGCTGGCGCGCGCAGGAGCCACAGT 4661
 RESULT 11
 US-11-121-086-27/c
 ; Sequence 27, Application US/11121086
 ; Publication No. US20050266459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: POULSEN, TIM S.
 ; APPLICANT: NIELSEN, KIRSTEN V.
 ; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
 ; FILE REFERENCE: 09138.6000-00000
 ; CURRENT APPLICATION NUMBER: US/11/121,086
 ; CURRENT FILING DATE: 2005-05-04
 ; PRIOR APPLICATION NUMBER: 60/567,570
 ; PRIOR FILING DATE: 2004-05-04
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 27
 ; LENGTH: 153142
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-121-086-27
 Alignment Scores:
 Pred. No.: 3,16e+04 Length: 153142
 Score: 82.50 Matches: 40
 Percent Similarity: 36.69% Conservative: 22
 Best Local Similarity: 23.67% Mismatches: 64
 Query Match: 4.72% Indels: 44

DB: 7 Gaps: 7

US-10-670-454-2 (1-331) x US-11-121-086-27 (1-153142)

QY 75 LysLysSerGlnSerGluLysAspArgAla----- 84

DB 72920 AGGAAATCACAGGGGAGCCAGCAGATCGTGAAACTTGGTGAATCTTTATTAATAACTAG 72861

QY 85 GlyProAspProPheGlyTyrGlySerLysArgIle----- 97

DB 72860 GGTCCACCCAGGAGCAGCGCTGGGCGGGGACAGGGTCTCCCGTGCAGGCTGCGCGGA 72801

QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrLeu 109

DB 72800 GGCAGGAGCCAGGGGTGGGTGGGTGCATGGCTGCAGGCTTCGGCGTTCAGTGATTG 72741

QY 110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129

DB 72740 TCGCTGGGCACAGGGCGCGCTGGTG---CCACGGCAGCCTGCACCTTCTCCACCAGC 72684

QY 130 ProHisPheArgAlaValValGluAsn----- 139

DB 72683 CCGGCCACTGGCTGCATGTCTTCCACAGGGGCTCGAACAGCTCTTGAGGGGGGCC 72624

QY 140 ---TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGly 158

DB 72623 TGGAGGCGCTCGGCTGCAGGCGTATCTCTGGGCC-----TGCTCTCCAG- 72577

QY 159 LeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178

DB 72576 CTTGGCGCGCAGCTCGCGCACCTGTCTCTTCACTCTGCAGCGGCTCGCGGTCCGGCT 72517

QY 179 CysPheArgLeuAsn-----HisTyrProCysProGluValGlnAlaLeuAsnArg 196

DB 72516 GGCATCTCTTCATCCGCGCGCGAGCGCTGCGCCCGGCTGGGCCCGCTCTGTAG 72457

QY 197 AsnLeuValGlyPheGlyGluHisThr 205

DB 72456 CGGCTGGCGCGCAGGAGCCACAGT 72430

RESULT 12

US-10-995-561-13513/c

; Sequence 13513, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13513

; LENGTH: 40000

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(40000)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-13513)

US-10-995-561-13513

Alignment Scores:

Pred. No.: 5,31e+03 Length: 40000

Score: 81.50 Matches: 40

Percent Similarity: 34.04% Conservative: 24

Best Local Similarity: 21.28% Mismatches: 69

Query Match: 4.66% Indels: 55

DB: 6 Gaps: 8

US-10-670-454-2 (1-331) x US-10-995-561-13513 (1-40000)

QY 75 LysLysSerGlnSerGluLysAspArgAla----- 84

DB 23840 AGGAAATCACAGGGGAGCCAGCAGATCGTGAAACTTGGTGAATCTTTATTAATAACTAG 23781

QY 85 GlyProAspProPheGlyTyrGlySerLysArgIle----- 97

DB 23780 GGTCCACCCAGGAGCAGCGCTGGGCGGGGACAGGGTCTCCCGTGCAGGCTGCGCGGA 23721

QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrLeu 109

DB 23720 GGCAGGAGCCAGGGGTGGGTGGGTGCATGGCTGCAGGCTTCGGCGTTCAGTGATTG 23661

QY 110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129

DB 23660 TCGCTGGGCACAGGGCGCGCTGGTG---CCACGGCAGCCTGCACCTTCTCCACCAGC 23604

QY 130 ProHisPheArgAlaValValGluAsn----- 139

DB 23603 CCGGCCACTGGCTGCATGTCTTCCACAGGGGCTCGAACAGCTCTTGAGGGGGGCC 23544

QY 140 ---TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGly 158

DB 23543 TGGAGGCGCTCGGCTGCAGGCGTATCTCTGGGCC-----TGCTCTCCAG- 23490

QY 159 LeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178

DB 23489 -----CGCACCTKCGCCACCTGCTCTTCCACCTCGTCCAGGCGGTG 23448

QY 179 CysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgLeu 198

DB 23447 CCGGCTCGGCTG-----GCCATCTCTCCATCCGCGCGCAGCGCTCGCCC 23400

QY 199 ValGlyPheGlyGluHis-----ThrAspProGlnIleIleSerVal 212

DB 23399 YAGGCTGGGCGCGCTCTGTAGCGGCTGGCGCGGAGGCCACAGTGGCGGGCCGC 23340

QY 213 LeuArgSerAsnSerThrSerGly 220

DB 23339 ACGCGGCCCTSTTCCACCAGGGGC 23316

RESULT 13

US-10-501-675-8

; Sequence 8, Application US/10501675

; Publication No. US20050282161A1

; GENERAL INFORMATION:

; APPLICANT: TANABE SEIYAKU CO., LTD.

; TITLE OF INVENTION: A Novel Phospholipase A2 and the gene thereof.

; FILE REFERENCE: 03-004-PCT

; CURRENT APPLICATION NUMBER: US/10/501,675

; CURRENT FILING DATE: 2004-07-16

; PRIOR APPLICATION NUMBER: JP2002-008435

; PRIOR FILING DATE: 2002-01-17

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 3587

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (99)..(2552)

; OTHER INFORMATION: (99)..(2552)

US-10-501-675-8

Alignment Scores:

Pred. No.: 150 Length: 3587

Score: 81.00 Matches: 69

Percent Similarity: 35.81% Conservative: 42

Best Local Similarity: 22.26% Mismatches: 104

Query Match: 4.63% Indels: 95

DB: 6 Gaps: 18

US-10-670-454-2 (1-331) x US-10-501-675-8 (1-3587)

APPLICANT: KERR, Richard


```
Db 712 GTCAAGGGCTGCTCTGTCAGCTTCTCTGAAGGAATACCTGTTACTCATAGATAGCCT 653
QY 279 Gly-----ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
Db 652 GGAGAGAGCTGAGCGCGCACTCTGCGTAAGGTTTGGCCCTGTAGCACCGTC----- 599
QY 295 LysGlyGluGluCysLeuTyrLysGlu-----PheThrTrpCys-----Glu 308
Db 598 -----TGCTTGGAAACAGGAAGCAGTGTCTCTGTTGTGTTTATAT 551
QY 309 TyrLysLysAlaAlaTyrThrSerArgLeu 318
Db 550 TTCAAGGCAACATGTCAACACAGTAACCTT 521
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RESULT 15

```
US-10-995-561-13294/c
; Sequence 13294, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13294
; LENGTH: 15804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(15804)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13294
```

Alignment Scores:

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Pred. No.: 1.69e+03 Length: 15804
Score: 80.50 Matches: 40
Percent Similarity: 34.04% Conservative: 24
Best Local Similarity: 21.28% Mismatches: 69
Query Match: 4.61% Indels: 55
DB: 6 Gaps: 8
```

US-10-670-454-2 (1-331) x US-10-995-561-13294 (1-15804)

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QY 75 LysLysSerGlnSerGluLysAspArgAla----- 84
Db 9829 AGGAATACAGGGGAGCGCCAGCAGATCGGTGAACCTTGGTGAATCTTTATTAAACTAG 9770
QY 85 GlyProAspProPheGlyTyrGlySerLysArgIle----- 97
Db 9769 GGTCCACCCAGGAGAGCGCTGGGGGGGACAGGGTCTCCCGTGCAGGCTGGCGGGA 9710
QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrLeu 109
Db 9709 GGCAGAGGACACGGGTGCGGTGGGGTGCATGGGTGCAGGCTTCGGCGTTGAGTGATTG 9650
QY 110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129
Db 9649 TCGCTGGGCACAGGGCGCGCTGGTG-----CCACGGCAGCTGCACCTTCTCCACCAGC 9593
QY 130 ProHisHisPheArgAlaValValGluAsn----- 139
Db 9592 CCGGCCCACTGGCGTGCATGTCTTCCACAGGGGCTCGAACCCAGCTCTTGAGGGGGGCC 9533
QY 140 ---TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGly 158
Db 9532 TGAAGGCCTCGGCCTGACGGCGTATCTGCTGGGCTGCTCTCTYACGCTTGGCG----- 9479
```

```
QY 159 LeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178
Db 9478 -----CGCACCTCCGCCACCTGCTCTTCACTCGTCCAGGCGGTGG 9437
QY 179 CysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeu 198
Db 9436 CGGGTCCGGCTG-----CCCATCTCTCCATCCGCGCGCGGACGCCGCTCGCCC 9389
QY 199 ValGlyPheGlyGluHis-----ThrAspProGlnIleIleSerVal 212
Db 9388 YAGGCTGGGCCCGCTCTCTGTAGCGGTGGCGGCCAGGAGCCACAGTGGCGGCCCGC 9329
QY 213 LeuArgSerAsnSerThrSerGly 220
Db 9328 ACGCGGCCCTSTTCCACCAGGGGC 9305
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Search completed: December 28, 2005, 05:19:57
Job time : 891 secs